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PTO/SB/05 (2/98)

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UTILITY PATENT APPLICATION TRANSMITTAL <i>(Only for new nonprovisional applications under 37 CFR 1.53(b))</i>		Attorney Docket No. 04983.0207.US00/38-10(15498)A	
		First Named Inventor or Application Identifier CAO	
		Title	Emericella Nidulans Genome Sequence and Uses Thereof
		Express Mail Label No.	

APPLICATION ELEMENTS <i>See MPEP chapter 600 concerning utility patent application contents</i>	ADDRESS TO: Assistant Commissioner for Patents Box Patent Application Washington, DC 20231
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<p>1. <input checked="" type="checkbox"/> *Fee Transmittal Form (Form PTO-1082) <i>(Submit an original and a duplicate for fee processing)</i></p> <p>2. <input checked="" type="checkbox"/> Specification [Total Pages 1686] <i>(preferred arrangement set forth below)</i></p> <ul style="list-style-type: none">- Descriptive title of the Invention- Cross References to Related Applications- Statement Regarding Fed sponsored R&D- Reference to Microfiche Appendix- Background of the Invention- Brief Summary of the Invention- Brief Description of the Drawings (if filed)- Detailed Description- Claims- Abstract of the Disclosure <p>3. <input type="checkbox"/> Drawing(s) (35 USC 113) [Total Sheets <input type="checkbox"/>]</p> <p>4. <input type="checkbox"/> Oath or Declaration [Total Pages <input type="checkbox"/>]</p> <p>a. <input type="checkbox"/> Newly executed (original or copy)</p> <p>b. <input type="checkbox"/> Copy from a prior application (37 CFR 1.63(d)) <i>(for continuation/divisional with Box 17 completed)</i> <i>[Note Box 5 below]</i></p> <p>i. <input type="checkbox"/> DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).</p> <p>5. <input type="checkbox"/> Incorporation By Reference <i>(useable if Box 4b is checked)</i> The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.</p>	<p>6. <input type="checkbox"/> Microfiche Computer Program <i>(Appendix)</i></p> <p>7. Nucleotide and/or Amino Acid Sequence Submission <i>(if applicable, all necessary)</i></p> <p>a. <input checked="" type="checkbox"/> Computer Readable Copy</p> <p>b. <input checked="" type="checkbox"/> Paper Copy (identical to computer copy)</p> <p>c. <input checked="" type="checkbox"/> Statement verifying identity of above copies</p>
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ACCOMPANYING APPLICATION PARTS	
<p>8. <input type="checkbox"/> Assignment Papers (cover sheet & document(s))</p> <p>9. <input type="checkbox"/> 37 CFR 3.73(b) Statement <input type="checkbox"/> Power of Attorney <i>(when there is an assignee)</i></p> <p>10. <input type="checkbox"/> English Translation Document <i>(if applicable)</i></p> <p>11. <input type="checkbox"/> Information Disclosure Statement (IDS)/PTO-1449 <input type="checkbox"/> Copies of IDS Citations</p> <p>12. <input type="checkbox"/> Preliminary Amendment</p> <p>13. <input checked="" type="checkbox"/> Return Receipt Postcard (MPEP 503) (Two) <i>(should be specifically itemized)</i></p> <p>14. <input type="checkbox"/> *Small Entity Statement(s) <input type="checkbox"/> Statement filed in prior application, Status still proper and desired</p> <p>15. <input type="checkbox"/> Certified Copy of Priority Document(s) <i>(if foreign priority is claimed)</i></p> <p>16. <input checked="" type="checkbox"/> Other: Statement Regarding Sequence Submission</p>	<p><small>*NOTE FOR ITEMS 1 & 14 IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).</small></p>

17. If a **CONTINUING APPLICATION**, check appropriate box and supply the requisite information:

☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No: /

Prior Application Information: Examiner: Group/Art Unit:

18. CORRESPONDENCE ADDRESS

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Attorney Docket No. 04983.0207.US00/38-10(15498)A

ASSISTANT COMMISSIONER FOR PATENTS
 Washington, DC 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventors: Yongwei CAO *et al.*

For: *Emericella Nidulans* Genome Sequence and Uses Thereof

Enclosed are:

- ☒ U.S. Utility Patent Application (consisting of 1,677 pages of description prior to the claims; 8 pages of claims, 1 page abstract and 31,579 pages of a sequence listing)
- ☒ CD-ROM containing the sequence listing
- ☒ Statement regarding Sequence Submission

This application is being filed without an executed Declaration.


The filing fee has been calculated as shown below:

(Col. 1)		(Col. 2)	SMALL ENTITY		OR	OTHER THAN A SMALL ENTITY	
FOR	NO. FILED	NO. EXTRA	RATE	FEE		RATE	FEE
BASIC FEE				365.00	OR		760.00
TOTAL CLAIMS	46 - 20 = *	26	x 9 =		OR	x 18 =	468.00
INDEP. CLAIMS	14 - 3 = *	11	x 39 =		OR	x 78 =	858.00
<input type="checkbox"/> MULTIPLE DEPENDENT CLAIM PRESENTED			+ 130 =		OR	+ 260 =	
			TOTAL	\$	OR	TOTAL	\$ 2086.00

*If the difference in Col. 1 is less than zero, enter "0" in Col. 2

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- ☒ Howrey & Simon Check No. 316494 in the amount of \$ 2,086.00 to cover the basic filing fee and extra claims fee is enclosed.
- ☒ The U.S. Patent and Trademark Office is hereby authorized to charge payment of the following fees associated with this communication or credit Any overpayment to Deposit Account No. 08-3038. A duplicate of this sheet is attached.
 - ☒ Any additional filing fees required under 37 C.F.R. § 1.16.
 - ☒ Any patent application processing fees under 37 C.F.R. § 1.17.
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 - ☐ Any patent application processing fees under 37 C.F.R. § 1.17.
 - ☐ The issue fee set in 37 C.F.R. § 1.18 at or before mailing of the Notice of Allowance, pursuant to 37 C.F.R. § 1.311(b).
 - ☐ Any filing fees under 37 C.F.R. § 1.16 for presentation of extra claims.

Date: September 23, 1999


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September 23, 1999

Box Patent Application

Assistant Commissioner for Patents
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Re: U.S. Non-Provisional Utility Patent Application
Application No.: To Be Assigned
Filed: Herewith
For: ***Emericella Nidulans* Genome Sequence
and Uses Thereof**
Inventors: Yongwei CAO *et al.*
Atty. Docket: 04983.0207.US00/38-10(15498)A

Sir:

The following documents are forwarded herewith for appropriate action by the U.S.
Patent and Trademark Office:

1. Utility Patent Application Transmittal (PTO/SB/05);
2. Form PTO-1082 (in duplicate);
3. U.S. Utility Patent Application entitled:

***Emericella Nidulans* Genome Sequence and Uses Thereof**

and naming as inventors:

**Yongwei CAO, Azita GHODSSI, Gregory J. HINKLE, James McININCH,
William E. TIMBERLAKE, and Jaehyuk YU**

the application consisting of:

- a. A specification containing:
 - (i) 1,677 pages of a description prior to the claims;
 - (ii) 8 pages of claims (46 claims);
 - (iii) a one (1) page abstract; and
 - (iv) 31,579 pages of a sequence listing;

- ## Enclosures

EMERICELLA NIDULANS GENOME SEQUENCE AND USES THEREOF

This application claims priority under 35 U.S.C §119(e) of U.S. Provisional Applications Nos. 60/ 101,665; 60/101,666; 60/102,358; 60/113,361; 60/126,265; 60/130,189; 60/130,190; 60/132,861; 60/138,103; and 60/149,882, the disclosures of which provisional applications are
5 incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

Included in the disclosure are nucleic acid molecules representing the genome of the filamentous fungus, *Emericella nidulans* (previously and still sometimes called *Aspergillus*
10 *nidulans*) and, in particular, to nucleic acid molecules having nucleic acid sequences corresponding to genes, promoters, other regulatory elements, and introns found in the *E. nidulans* genome, a specific set of genes of *E. nidulans* and a set of primers based on the *E. nidulans* genes. Also disclosed are homologous nucleic acid molecules, complementary nucleic acid molecules, polypeptides expressed by such genes, constructs comprising such promoters,
15 regulatory elements and/or genes, transformed cells and organisms comprising such genes and/or promoters and regulatory elements, primers useful for replicating parts of such genes and nucleic acid molecules, computer readable media comprising sets of such nucleic acid sequences, polypeptides and primers, collections of nucleic acid molecules and methods of using such molecules and sequences including the use of collections of nucleic acid molecules in genetic
20 research and clinical analysis, *e.g.* for gene expression.

BACKGROUND OF THE INVENTION

Filamentous fungi have a complex multicellular organization involving production of highly specialized cell types as part of their normal asexual and sexual lifecycles. Fungi as experimental systems are good models for plant and animal cell functions because of their evolutionary relatedness. *E. nidulans* is a model eukaryotic organism and has been used extensively to address fundamental questions of biology. *E. nidulans* is a more complex organism than yeast and has many genes which have a similar function to genes found in plants and animals. This filamentous fungus has been employed in investigations into a variety of genetic phenomena including the mechanisms regulating carbon and nitrogen metabolism, cell cycle, cytoskeletal functions, and development. A set of nucleic acid molecules representing substantially most of the genes in the *E. nidulans* genome is useful in transcription profiling work to find, identify and characterize counterpart genes in other species, particularly microbial and plant species. For instance, it is possible to identify unknown plant gene function by studying a similar (homologous) gene in a microbe in which genetic modification can more easily be done. That is, if unknown genes are disrupted or overexpressed, transcription profiling can be carried out to understand effects of the genetic modification.

Moreover, chemical/drug discovery can be practiced using such transcription profiling with nucleic acids molecules of the *E. nidulans* genome. And, because many human or plant pathogens are filamentous fungi and *E. nidulans* is a model organism for filamentous fungi, transcription profiling with genome-wide expression of the *E. nidulans* genome is an efficient way to understand the action of such pathogens and their secondary metabolites, *e.g.* mycotoxins which can be deleterious to food and feed supplies. In addition environmental stress studies of

the *E. nidulans* genome will provide insight into related mechanisms in plants, *e.g.* yield, stability, thermal resistance, water/drought tolerance, *etc.*

Nucleic acid molecules comprising the *E. nidulans* genome disclosed herein were identified and isolated from a sample of filamentous fungus identified as *Aspergillus nidulans*,

5 FGSC Number A4, obtained from the Fungal Genetics Stock Center (FGSC) at the University of Kansas Medical Center, Kansas City, Kansas. It has been determined that this fungus is more properly named *Emericella nidulans*. As used herein the terms *Emericella nidulans*, *E. nidulans*, *Aspergillus nidulans* and *A. nidulans* refer to the filamentous fungus previously and still sometimes called *Aspergillus nidulans*.

10 Nucleic acid sequences of a species, *e.g.* the *E. nidulans*, can be generated by random shotgun sequencing of cloned genomic DNA and assembled into longer lengths of contiguous sequence (contigs). The final data set from an assembly process comprises a collection of sequences, which includes the contigs resulting from linking of two or more overlapping sequences as well as singleton nucleic acid sequences, *i.e.* trace sequences which are not
15 incorporated into contigs. Such sequences can be screened for genes, *e.g.* full length or substantially full length or partial length genes. Screening methods include homology searches against databases of known genes and predictive methods using algorithms which infer the presence and extent of a gene.

The nucleic acid sequences disclosed herein are believed to represent substantially all, or
20 at least a major part, of the genes in the *E. nidulans* genome. Genome sequence information from *E. nidulans* permits identification of genetic sequences from other organisms, including plants, mammals such as humans, bacteria, other filamentous fungi and non-filamentous fungi such as a yeast, *e.g.* by comparison of such sequences with *E. nidulans* sequences. The

availability of a substantially complete set genes or partial genes of the *E. nidulans* genome permits the definition of primers for fabricating representative nucleic acid molecules of the genome which can be used on microarrays facilitating transcription profile studies. In addition the identification of the *E. nidulans* genome permits the fabrication of a wide variety of DNA constructs useful for imparting unique genetic properties into transgenic organisms. These and other advantages attendant with the various aspects of this invention will be apparent from the following description of the invention and its various embodiments.

SUMMARY OF THE INVENTION

The present invention contemplates and provides a substantial part of the genome of the filamentous fungus *Emericella nidulans*. One aspect of the invention is a set of more than 16,000 contig and singleton sequences comprising coding sequence as well as promoters, other regulatory elements and introns represented by SEQ ID NO: 1 through SEQ ID NO: 16206. Contigs in SEQ ID NO: 1 through SEQ ID NO: 16206 are recognized as those sequences whose designations begin with ANI61C or ANI50C. Singleton sequences are recognized as those having designations which begin with ANI61S or ANI50S. Thus, a subset of the nucleic acid molecules of this invention comprises promoters and/or other regulatory elements of the *E. nidulans* genome as present in SEQ ID NO: 1 through SEQ ID NO: 16206 or complements thereof.

Another aspect of this invention comprises a set of about 12,000 genes or partial genes of the *E. nidulans* genome including genes represented by SEQ ID NO: 16207 through SEQ ID NO: 27905 and a small set of previously reported genes represented by SEQ ID NO: 27906 through SEQ ID NO: 28165. As used herein, a substantially complete set of genes for an

organism is referred to as a unigene set. Thus, as used herein reference is made to specific genes comprising the unigene set of *E. nidulans* as “ENUxxxxx” where ENU is an acronym for *Emericella nidulans unigene* and xxxxx represents a number. Thus, ENU00001 to ENU27905 are used to designate the genes of *E. nidulans* identified herein; and, ENU27906 to ENU28165 are used to designate the previously reported genes of *E. nidulans*. Moreover, the term “ENU” by itself is also used herein to mean any of the nucleic acid molecules comprising genes or partial genes of the unigene set for *E. nidulans*. More particularly the term “ENU of this invention” as used herein means a nucleic acid molecule representing a gene or partial gene of *E. nidulans* disclosed herein selected from the group consisting of ENU00001 to ENU27905.

The present invention also contemplates and provides substantially purified nucleic acid molecules comprising the ENUs and other nucleic acid molecules of this invention as well as molecules which are complementary to, and capable of specifically hybridizing to, the ENU or its complement.

The present invention also contemplates and provides substantially purified nucleic acids molecules which are homologous to the nucleic acid molecules of this invention including, for example, those which are homologous to the ENUs of this invention, *e.g.* a plurality of related sets of homologous nucleic acid molecules in other species which are homologous to the ENUs.

The present invention also contemplates and provides substantially purified protein, or polypeptide fragments thereof, which are encoded by cDNA associated with the ENUs of the present invention.

The present invention also contemplates and provides constructs comprising promoters, regulatory elements and/or the ENUs which are useful in making transgenic cells or organisms. In particular this invention also provides transformed cell or organism having a nucleic acid

molecule which comprises: (a) a promoter region which functions in the cell to cause the production of a mRNA molecule; which is linked to (b) a structural nucleic acid molecule, which is linked to (c) a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule, where components (a) and/or (b) are selected from *E. nidulans* nucleic acid sequences provided herein and more preferably selected *E. nidulans* nucleic acid sequences from the group consisting of ENU00001 to ENU27905.

Still another aspect of this invention is a set (and subsets thereof) of about 24,000 primers for the ENUs of this invention, including a specific subset of about 16,000 primers represented by SEQ ID NO: 28166 through SEQ ID NO: 44345 which can be used to generate and isolate nucleic acid molecules representative ENUs of this invention and homologs thereof in other non-*E. Nidulans* species. The nucleic acids molecules of this invention including primers represent a useful tool in genetic research not only for the species *E. nidulans*, but also for other fungal species, other microorganisms and life forms with more differentiated cell structure such as plants and animals. The present invention also contemplates and provides primer pairs for replicating or identifying parts of the ENUs.

The present invention also contemplates and provides computer readable media having recorded thereon one or more of the nucleotide sequences provided by this invention and methods for using such media, *e.g.* in searching to identify genes associated with nucleic acid sequences.

The present invention also contemplates and provides collections of nucleic acid molecules, including oligonucleotides, representing the *E. nidulans* genome including collections on solid substrates, *e.g.* substrates having attached thereto in array form nucleic acid molecules

or oligonucleotides representing genes of the *E. nidulans* genome. The invention also contemplates and provides methods of using such collections and arrays, *e.g.* in transcription profiling analysis. The present invention also contemplates and provides methods for using the nucleic acid molecules of this invention, *e.g.* for identifying genetic material and/or determining gene expression by hybridizing expressed and labeled nucleic acid molecules or fragments thereof to arrayed collections of the nucleic acid molecules of this invention.

The present invention also contemplates and provides oligonucleotides which are identical or complementary to a sequence of similar length for an ENU. Such oligonucleotides are useful, for example, for hybridizing to and identifying nucleic acid molecules which are homologous and/or complementary to the ENUs of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

As used herein, a nucleic acid molecule and/or polypeptide molecule, be it a naturally occurring molecule or otherwise, may be “substantially purified”, if the molecule is separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term “substantially purified” is not intended to encompass molecules present in their native state.

The ENUs of this invention and other nucleic acid molecules and/or polypeptide molecules of the present invention will preferably be “biologically active” with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid

molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

As used herein the term "polypeptide" means a protein or fragment thereof expressed by a nucleic acid molecule in a cell.

The ENUs of this invention and other nucleic acid molecules of the present invention may also be recombinant. As used herein, the term recombinant means any molecule (*e.g.* DNA, peptide *etc.*), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the nucleic acid molecules of the present invention may be labeled with reagents that facilitate detection of the agent, *e.g.* fluorescent labels as disclosed in US Patent 4,653,417, chemical labels as disclosed in U.S. Patents 4,582,789 and 4,563,417 and modified bases as disclosed in US Patent 4,605,735, all of which are incorporated herein by reference in their entirety.

The term "oligonucleotide" as used herein refers to short nucleic acid molecules useful, *e.g.* for hybridizing probes, nucleotide array elements or amplification primers. Oligonucleotide molecules are comprised of two or more nucleotides, *i.e.* deoxyribonucleotides or ribonucleotides, preferably more than five and up to 30 or more. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide.

Oligonucleotides can comprise ligated natural nucleic molecules acids or synthesized nucleic acid molecules and comprise between 5 to 150 nucleotides or between about 15 and about 100 nucleotides, or preferably up to 100 nucleotides, and even more preferably between 15 to 30

nucleotides or most preferably between 18-25 nucleotides, identical or complementary to a sequence of similar length for an ENU.

This invention provides oligonucleotides specific for ENU sequences. Such oligonucleotides may be nucleic acid elements for use on solid arrays (*e.g.* synthesized or spotted) or primers for amplification of ENUs of this invention. Such primers for use in polymerase chain reaction (PCR) primers are preferably designed with the goal of amplifying nucleic acids from either the 3' or the 5' end of an ENU or a fragment of an ENU, *e.g.* about 500 to 800 bp of nucleic acids from the at the 3' end of such a nucleic acid molecule.

The term "primer" as used herein refers to a nucleic acid molecule, preferably an oligonucleotide whether derived from a naturally occurring molecule, such as one isolated from a restriction digest or one produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, *i.e.*, in the presence of nucleotides and an agent for polymerization such as DNA polymerase and at a suitable temperature and pH.

The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the agent for polymerization. The exact lengths of the primers will depend on many factors, including temperature and source of primer. For example, depending on the complexity of the target sequence, the oligonucleotide primer typically contains at least 15, more preferably 18 nucleotides, which are identical or complementary to the template and optionally a tail of variable length which need not match the template. The length

of the tail should not be so long that it interferes with the recognition of the template. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

The primers herein are selected to be "substantially" complementary to the different

5 strands of each specific sequence to be amplified. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the
10 primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and thereby form a template for synthesis of the extension product of the other primer. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STSPipeline), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998)), for
15 example, can be used to identify potential PCR primers. Exemplary primers include primers that are 18 to 50 bases long, where at least between 18 to 25 bases are identical or complementary to at least 18 to 25 bases segment of the template sequence. Preferred template sequences for such primers are selected from a fragment of any one of SEQ ID NO: 16207 through SEQ ID NO:
20 28905 or complements thereof.

This invention also contemplates and provides primer pairs for amplification of nucleic acid molecules representing the ENUs. As used herein "primer pair" means a set of two oligonucleotide primers based on two separated sequence segments of a target nucleic acid

sequence. One primer of the pair is a “forward primer” or “5’ primer” having a sequence which is identical to the more 5’ of the separated sequence segments. The other primer of the pair is a “reverse primer” or “3’ primer” having a sequence which is complementary to the more 3’ of the separated sequence segments. A primer pair allows for amplification of the nucleic acid

5 sequence between and including the separated sequence segments. Optionally, each primer pair can comprise additional sequences, *e.g.* universal primer sequences or restriction endonuclease sites, at the 5’ end of each primer, *e.g.* to facilitate cloning, DNA sequencing, or reamplification of the target nucleic acid sequence.

Nucleic acid molecules of the present invention include those having a nucleic acid
 10 sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 44,435 and complements thereof and fragments of either. Preferred nucleic acid molecules include those having a nucleic acid sequence selected from the following groups: SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 26804 or complements thereof; SEQ ID NO: 26000 through SEQ ID NO: 26804 or complements thereof;
 15 SEQ ID NO: 16207 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 24035 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 22710 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 22709 or complements thereof; ; SEQ ID NO: 17681 through SEQ ID NO: 22709 or complements thereof; SEQ ID NO: 16207 through SEQ ID
 20 NO: 17680 or complements thereof; SEQ ID NO: 17618 through SEQ ID NO: 17680 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 17295 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17294 or complements thereof. Other preferred nucleic acid molecules

include any of the above groups but where such groups also include fragments of such sequences.

Nucleic acid molecules or fragments thereof are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure along a sufficient portion of the molecule to allow for stable binding under laboratory hybridizing conditions. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning*, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), and by Haymes *et al.*, *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985), the entirety of both of which are herein incorporated by reference. Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be

sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency of about 0.2 X SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

Preferred embodiments of the nucleic acid of this invention will specifically hybridize to one or more of the ENUs of this invention or complements thereof under low stringency conditions, for example at about 2.0 X SSC and about 50°C. In a particularly preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the ENUs of this invention or complements thereof under moderate stringency conditions. In an especially preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the ENUs of this invention or complements thereof under high stringency conditions.

In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 90% sequence identity with one or more of the ENUs of this invention or complements thereof. In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 95%

sequence identity with one or more of the ENUs of this invention or complements thereof. In a more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 98% sequence identity with one or more of the ENUs of this invention or complements thereof. In an even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 99% sequence identity with one or more of the ENUs of this invention or complements thereof.

The present invention also encompasses the use of nucleic acids of the present invention in recombinant constructs. Using methods known to those of ordinary skill in the art, an ENU sequence and/or a promoter sequence of the invention can be inserted into constructs which can be introduced into a host cell of choice for expression of the encoded protein if an ENU is used or for use of an *E. nidulans* promoter to direct expression of a heterologous protein. Potential host cells include both prokaryotic and eukaryotic cells. A host cell may be unicellular or found in a multicellular differentiated or undifferentiated organism depending upon the intended use. It is understood that useful exogenous genetic material may be introduced into any non-fungal cell or organism such as a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird or bacterial cell.

Depending upon the host, the regulatory regions for expression of ENU sequences will vary, including regions from viral, plasmid or chromosomal genes, or the like. For expression in prokaryotic or eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or regulatable promoters may be employed. Among transcriptional initiation regions which have been described are regions from bacterial and yeast hosts, such as *E. coli*, *B. subtilis*, *Saccharomyces cerevisiae*, including genes such as beta-galactosidase, T7 polymerase and

tryptophan E.

Furthermore, for use in transformation of *E. nidulans*, constructs may include those in which an ENU sequence or portion thereof of the present invention is positioned with respect to a promoter sequence such that production of antisense mRNA complementary to native mRNA molecules is provided. In this manner, expression of the native gene may be decreased. Such methods may find use for modification of particular functions of the targeted host, and/or for discovering the function of a protein naturally expressed in *E. nidulans*.

Complements and homologs of ENUs

Another embodiment of the present invention comprises a nucleic acid molecule which is a homolog of an ENU of this invention which encodes a polypeptide also found in a plant, animal or bacterial organism. Yet another embodiment comprises a nucleic acid molecule which encodes a polypeptide which is homologous to a polypeptide encoded by an ENU of this invention where the percent identity between the polypeptides is between about 25% and about 40%, more preferably of between about 40 and about 70%, even more preferably of between about 70% and about 90%, and even more preferably between about 90% and 99% and most preferably 100%.

Genomic sequences can be screened for the presence of protein homologs utilizing one or a number of different search algorithms that have been developed, one example of which are the suite of programs referred to as BLAST programs. In addition, unidentified reading frames may be screened for by gene prediction software such as GenScan available for downloading from the Stanford University web site. The degeneracy of the genetic code allows different nucleic acid sequences to code for the same protein or peptide, *e.g. see* U.S. Patent No. 4,757,006, the entirety

of which is herein incorporated by reference. As used herein a nucleic acid molecule is degenerate of another nucleic acid molecule when the nucleic acid molecules encode for the same amino acid sequences but comprise different nucleotide sequences. An aspect of the present invention is that the nucleic acid molecules of the present invention include nucleic acid molecules that are degenerate from the ENUs of this invention.

A further aspect of the present invention comprises one or more nucleic acid molecules which differ in nucleic acid sequence from those of an ENU of this invention due to the degeneracy in the genetic code in that they encode the same protein but differ in nucleic acid sequence or a protein having one or more conservative amino acid residue. Codons capable of coding for such conservative substitutions are known in the art. For instance, serine is a conservative substitute of alanine and threonine is a conservative substitute for serine.

Regulatory Elements

One class of agents of the present invention includes nucleic acid molecules having promoter regions or partial promoter regions or other regulatory elements, particularly those found in SEQ ID NO: 1 through SEQ ID NO: 16144 and located upstream of the trinucleotide ATG sequence at the start site of a protein coding region. As used herein, a promoter region is a region of a nucleic acid molecule that is capable, when located in *cis* to a nucleic acid sequence that encodes for a protein or peptide to function in a way that directs expression of one or more mRNA molecules that encodes for the protein or peptide. Promoters of the present invention can comprise nucleic acids in the range from about 300 bp to at least 1000 bp or more, say about 2000 bp or even higher say about 5000 bp and up to about 10 kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. While in many circumstances a 300 bp

promoter may be sufficient for expression, additional sequences may act to further regulate expression, for example, in response to biochemical, developmental or environmental signals. In a preferred embodiment of the present invention, the promoter is upstream of a nucleic acid sequence that encodes an *E. nidulans* protein homolog or fragment thereof or preferably

5 upstream of an ENU of this invention. It is also preferred that the promoters of the present invention contain a CAAT and a TATA *cis* element. Moreover, the promoters of the present invention can include one or more *cis* elements in addition to a CAAT and a TATA box. For the most part, the promoters of the present invention will be located in contig sequences which generally represent longer nucleic acids than do singleton sequences of the present invention.

10 Contigs in SEQ ID NO:1 through SEQ ID NO:16144 are recognized as those sequences whose designations begin with ANI61C or ANI50C, as opposed to singletons whose designations begin with ANI61S or ANI50S. Where an ENU is specified as being located on two different contigs, the promoter region will be located on the contig representing the 5' region of the gene encoding sequence.

15 By "regulatory element" it is intended a series of nucleotides that determines if, when, and at what level a particular gene is expressed. The regulatory DNA sequences specifically interact with regulatory or other proteins. Many regulatory elements act in *cis* ("*cis* elements") and are believed to affect DNA topology, producing local conformations that selectively allow or restrict access of RNA polymerase to the DNA template or that facilitate selective opening of the

20 double helix at the site of transcriptional initiation. *Cis* elements occur within, but are not limited to promoters, and promoter modulating sequences (inducible elements). *Cis* elements can be identified using known *cis* elements as a target sequence or target motif in the BLAST programs of the present invention. Promoters of the present invention include homologs of *cis*

elements known to effect gene regulation that show homology with the nucleic acid molecules of the present invention.

Polypeptides

Other aspects of this invention comprises one or more of the polypeptides, including proteins or peptide molecules, encoded by the coding region of an ENU of this invention or fragments thereof or homologs thereof. Protein and peptide molecules can be identified using known protein or peptide molecules as a target sequence or target motif in the BLAST programs of the present invention. In a preferred embodiment the protein or fragment molecules of the present invention are derived from *E. nidulans*.

As used herein, the term “protein molecule” or “peptide molecule” includes any molecule that comprises five or more amino acids. It is well known in the art that proteins or peptides may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term “protein molecule” or “peptide molecule” includes any protein molecule that is modified by any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, ornithine, homocysteine, and homoserine.

One or more of the protein or peptide molecules may be produced via chemical synthesis, or more preferably, by expression in a suitable bacterial or eukaryotic host. Suitable methods for expression are described by Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual, 2nd Edition*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), or similar texts.

A “protein fragment” comprises a subset of the amino acid sequence of that protein. A protein fragment which comprises one or more additional peptide regions not derived from a

base protein is a “fusion” protein. Such molecules may be derivatized to contain carbohydrate or other groups (such as keyhole limpet hemocyanin, *etc.*). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprises protein or peptide molecules encoded by the coding
 5 region of an ENU of this invention or complements thereof or, fragments or fusions thereof in which conservative, non-essential, or not relevant, amino acid residues have been added, replaced, or deleted. An example of such a homolog is the homolog protein of a non-*E. nidulans* filamentous fungus. Such a homolog can be obtained by any of a variety of methods. For example, as indicated above, one or more of the disclosed sequences for primers of this invention
 10 can be used to define a pair of primers that may be used to isolate the homolog-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield homologs by recombinant means.

Antibodies

One aspect of the present invention concerns antibodies, single-chain antigen binding
 15 molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the present invention and their homologs, fusions or fragments. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the present invention. As used herein, an antibody or peptide is said to “specifically bind” to a protein or peptide molecule of the present invention if such binding is not competitively inhibited
 20 by the presence of non-related molecules. In a preferred embodiment the antibodies of the present invention bind to proteins of the present invention, in a more preferred embodiment of the antibodies of the present invention bind to proteins derived from *E. nidulans*.

Nucleic acid molecules that encode all or part of the protein of the present invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may be a “fusion” molecule (*i.e.*, a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the present invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the present invention may be polyclonal or monoclonal. It is understood that practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of antibodies (see, for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1988), the entirety of which is herein incorporated by reference).

It is understood that any of the antibodies of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Fungal Constructs and Fungal Transformants

The present invention also relates to a fungal recombinant vector, *e.g.* comprising exogenous genetic material. In a preferred embodiment the exogenous genetic material includes at least one nucleic acid molecule of the present invention which can preferably be (a) an ENU of this invention or fragment or homolog thereof or (b) a regulatory element, promoter or partial promoter of the present invention. In a further more preferred embodiment of the present invention exogenous genetic material includes a regulatory element, promoter or partial promoter

of the present invention and a nucleic acid molecule of the present invention having a sequence within a contig selected from the group identified by SEQ ID NO: 1 through SEQ ID NO: 16206 or complements thereof or fragments of either. In a further more preferred embodiment of the present invention exogenous genetic material includes a regulatory element, promoter or partial promoter of the present invention and a nucleic acid molecule encoding an *E. nidulans* protein homolog or fragments thereof. It is also understood that such exogenous genetic material may be introduced into any non-fungal cell or organism such as a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird or bacterial cell.

The recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host.

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like. The selectable marker may be selected from the group including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hygB* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), *trpC* (anthranilate synthase) and *gfp* (green fluorescent protein). Preferred for use in an *Emericella* cell are the *amdS* and *pyrG* markers of *Emericella nidulans* or *Aspergillus, oryzae* and the *bar* marker of

Streptomyces hygroscopicus. Furthermore, selection may be accomplished by co-transformation, e.g., as described in WO 91/17243, the entirety of which is herein incorporated by reference.

A nucleic acid sequence of the present invention may be operably linked to a suitable promoter sequence. A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof, and to minimize the amount of possible degradation of the expressed protein or fragment thereof within the cell, it may be preferred that expression of the protein or fragment thereof gives rise to a product secreted outside the cell, especially in the case of expression in host cells of fungus or bacteria. To this end, the protein or fragment thereof of the present invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an amino acid sequence which permits the secretion of the protein or fragment thereof from the host into the culture medium.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be linked to a propeptide coding region. A propeptide is an amino acid sequence found at the amino terminus of a proprotein or proenzyme. Cleavage of the propeptide from the proprotein yields a mature biochemically active protein. The resulting polypeptide is known as a

propolypeptide or proenzyme (or a zymogen in some cases). Propolypeptides are generally inactive and can be converted to mature active polypeptides by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide or proenzyme. The propeptide coding region may be native to the protein or fragment thereof or may be obtained from foreign sources.

5 The expressed protein or fragment thereof may be detected using methods known in the art that are specific for the particular protein or fragment. These detection methods may include the use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, if the protein or fragment thereof has enzymatic activity, an enzyme assay may be used. Alternatively, if polyclonal or monoclonal antibodies specific to the protein
10 or fragment thereof are available, immunoassays may be employed using the antibodies to the protein or fragment thereof. The techniques of enzyme assay and immunoassay are well known to those skilled in the art.

 The resulting protein or fragment thereof may be recovered by methods known in the arts. For example, the protein or fragment thereof may be recovered from the nutrient medium by
15 conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. The recovered protein or fragment thereof may then be further purified by a variety of chromatographic procedures, *e.g.*, ion exchange chromatography, gel filtration chromatography, affinity chromatography, or the like.

Plant Constructs and Plant Transformants

20 ENUs or other nucleic acid molecules of this invention may be used in plant transformation or transfection. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of

being inserted into any organism. Such genetic material may be transferred into either monocotyledons and dicotyledons including but not limited to the plants, alfalfa, *Arabidopsis thaliana*, barley, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, maize, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, soybean, strawberry, 5 sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *etc.*

Exogenous genetic material may be transferred into a plant cell by the use of a DNA vector or construct designed for such a purpose. Vectors have been engineered for transformation of large DNA inserts into plant genomes. Binary bacterial artificial chromosomes 10 have been designed to replicate in both *E. coli* and *Agrobacterium tumefaciens* and have all of the features required for transferring large inserts of DNA into plant chromosomes. BAC vectors, *e.g.* a pBACwich, have been developed to achieve site-directed integration of DNA into a genome.

A construct or vector may also include a plant promoter to express the protein or protein 15 fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter, the octopine synthase (OCS) promoter, a caulimovirus promoter such as the CaMV 19S promoter and the CaMV 35S promoter, the figwort mosaic virus 35S promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate carboxylase (ssRUBISCO), the Adh promoter, the sucrose 20 synthase promoter, the R gene complex promoter, and the chlorophyll a/b binding protein gene promoter. For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of

promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea, the chloroplast fructose-1,6-biphosphatase (FBPase) promoter from wheat, the nuclear photosynthetic ST-LS1 promoter from potato, the phenylalanine ammonia-lyase (PAL) promoter and the chalcone synthase (CHS) promoter from *Arabidopsis thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, *cab6*, from pine, the promoter for the *Cab-1* gene from wheat, the promoter for the *CAB-1* gene from spinach, the promoter for the *cab1R* gene from rice, the pyruvate, orthophosphate dikinase (PPDK) promoter from *Zea mays*, the promoter for the tobacco *Lhcb1*2* gene, the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter, and the promoter for the thylacoid membrane proteins from spinach (*psaD*, *psaF*, *psaE*, *PC*, *FNR*, *atpC*, *atpD*, *cab*, *rbcS*). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the present invention, such as the promoters for *LhcB* gene and *PsbP* gene from white mustard (*Sinapis alba*). Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435 and 4,633,436, all of which are herein incorporated in their entirety.

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the nos 3' sequence or the like. It is understood that one or more sequences of the present invention that act to terminate transcription may be used.

A vector or construct may also include other regulatory elements or selectable markers.

Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, *etc.*; a bar gene which
 5 codes for bialaphos resistance; a mutant EPSP synthase gene which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil, a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance; and a methotrexate resistant DHFR gene.

A vector or construct may also include a screenable marker to monitor expression.

10 Exemplary screenable markers include a β -glucuronidase or uidA gene (GUS), an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a β -lactamase gene, a gene which encodes an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a luciferase gene, a xyle gene which encodes a catechol dioxygenase that can convert chromogenic
 15 catechols; an α -amylase gene, a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α -galactosidase, which will turn a chromogenic α -galactose substrate. Included within the terms “selectable or screenable marker genes” are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include
 20 markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, *e.g.*, by ELISA, small active enzymes detectable in extracellular solution (*e.g.*, α -amylase, β -lactamase, phosphinothricin transferase),

or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

Technology for introduction of DNA into cells is well known to those of skill in the art.

- 5 Four general methods for delivering a gene into cells have been described: (1) chemical methods, (2) physical methods such as microinjection and bombardment, (3) viral vectors and (4) receptor-mediated mechanisms.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes.

- 10 The present invention also provides for parts of the plants of the present invention. Plant parts, without limitation, include seed, endosperm, ovule and pollen. In a particularly preferred embodiment of the present invention, the plant part is a seed.

- 15 Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these treatments.

- Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters enhancers *etc.* Further any of the nucleic acid molecules encoding an *E. nidulans* protein or fragment thereof or homologs of the present invention may be introduced
20 into a plant cell in a manner that allows for over expression of the protein or fragment thereof encoded by the nucleic acid molecule.

Uses of the Agents of the Present Invention

Nucleic acid molecules of the present invention may be employed to obtain *other E. nidulans* nucleic acid molecules. Such molecules can be readily obtained by using the above-described nucleic acid molecules to screen *E. nidulans* libraries.

5 Nucleic acid molecules and fragments thereof of the present invention may also be employed to obtain nucleic acid molecule homologs of non-*E. nidulans* species including the nucleic acid molecules that encode, in whole or in part, protein homologs of other species or other organisms, sequences of genetic elements such as promoters and transcriptional regulatory elements. Such molecules can be readily obtained by using the above-described nucleic acid
10 molecules to screen cDNA or genomic libraries of non-*E. nidulans* species. Methods for forming such libraries are well known in the art. Such homolog molecules may differ in their nucleotide sequences from those found in one or more of the *E. nidulans* genes of this invention or complements thereof because complete complementarity is not needed for stable hybridization. The nucleic acid molecules of the present invention therefore also include molecules that,
15 although capable of specifically hybridizing with the nucleic acid molecules may lack “complete complementarity.”

The disclosed nucleic acid molecules may be used to define one or more primer pairs that can be used with the polymerase chain reaction to amplify and obtain any desired nucleic acid molecule or fragment thereof. Such molecules will find particular use in generation of nucleic
20 acid arrays, including microarrays, containing portions of or the entire encoding region for the identified *E. nidulans* genes. It is noted that the molecules on such arrays may contain native intervening sequences (introns) of the genes and will still find use in microarray based methods

such as transcriptional profiling for functional analysis of *E. nidulans* genes and metabolic pathways. Particularly preferred primers are those set forth in table 3.

The nucleic acid molecules of the present invention may be used for physical mapping. Physical mapping, in conjunction with linkage analysis, can enable the isolation of genes.

- 5 Physical mapping has been reported to identify the markers closest in terms of genetic recombination to a gene target for cloning. Once a DNA marker is linked to a gene of interest, the chromosome walking technique can be used to find the genes via overlapping clones. For chromosome walking, random molecular markers or established molecular linkage maps are used to conduct a search to localize the gene adjacent to one or more markers. A chromosome walk is then initiated from the closest linked marker. Starting from the selected clones, labeled probes specific for the ends of the insert DNA are synthesized and used as probes in hybridizations against a representative library. Clones hybridizing with one of the probes are picked and serve as templates for the synthesis of new probes; by subsequent analysis, contigs are produced.

- 15 The degree of overlap of the hybridizing clones used to produce a contig can be determined by comparative restriction analysis. Comparative restriction analysis can be carried out in different ways all of which exploit the same principle; two clones of a library are very likely to overlap if they contain a limited number of restriction sites for one or more restriction endonucleases located at the same distance from each other. The most frequently used procedures are, fingerprinting, restriction fragment mapping or the "landmarking" technique. It is understood that the nucleic acid molecules of the present invention may in one embodiment be used in physical mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used in the physical mapping of *E. nidulans*.

Nucleic acid molecules of the present invention can be used in comparative mapping.

Comparative mapping within families provides a method to assess the degree of sequence conservation, gene order, ploidy of species, ancestral relationships and the rates at which individual genomes are evolving. Comparative mapping has been carried out by cross-

5 hybridizing molecular markers across species within a given family. As in genetic mapping, molecular markers are needed but instead of direct hybridization to mapping filters, the markers are used to select large insert clones from a total genomic DNA library of a related species. The selected clones, each a representative of a single marker, can then be used to physically map the region in the target species. The advantage of this method for comparative mapping is that no
10 mapping population or linkage map of the target species is needed and the clones may also be used in other closely related species. By comparing the results obtained by genetic mapping in model organisms, with those from other species, similarities of genomic structure among species can be established. Cross-hybridization of RFLP markers has been reported and conserved gene order has been established in many studies. Such macroscopic synteny is utilized for the
15 estimation of correspondence of loci among these organisms. It is understood that nuclear acid molecules of the present invention may in another embodiment be used in comparative mapping. In a preferred embodiment the nucleic acid molecules of present invention may be used in the comparative mapping of filamentous fungi.

In an aspect of the present invention, one or more of the agents of the present invention
20 may be used to detecting the presence, absence or level of a organism, preferably a filamentous fungus and more preferably an *E. nidulans* in a sample. In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention are used to determine the level (*i.e.*, the concentration of mRNA in a sample, *etc.*) or pattern (*i.e.*, the

kinetics of expression, rate of decomposition, stability profile, *etc.*) of the expression of a protein encoded in part or whole by one or more of the nucleic acid molecule of the present invention (collectively, the “Expression Response” of a cell or tissue). As used herein, the Expression Response manifested by a cell or tissue is said to be “altered” if it differs from the Expression Response of cells or tissues of organisms not exhibiting the phenotype. To determine whether a Expression Response is altered, the Expression Response manifested by the cell or tissue of the organism exhibiting the phenotype is compared with that of a similar cell or tissue sample of a organism not exhibiting the phenotype. As will be appreciated, it is not necessary to re-determine the Expression Response of the cell or tissue sample of organisms not exhibiting the phenotype each time such a comparison is made; rather, the Expression Response of a particular organism may be compared with previously obtained values of normal organism. As used herein, the phenotype of the organism is any of one or more characteristics of an organism.

Nucleic acid molecules of the present invention can be used to monitor expression. A microarray-based method for high-throughput monitoring of gene expression may be utilized to measure gene-specific hybridization targets. This ‘chip’-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding genes. Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several methods have been described for fabricating microarrays of nucleic acid molecules and using such microarrays in detecting nucleic acid sequences. For instance, microarrays can be fabricated by spotting nucleic acid molecules, *e.g.* genes, oligonucleotides, *etc.*, onto substrates or fabricating oligonucleotide sequences in situ on a substrate. Spotted or fabricated nucleic acid molecules can be applied in a high density matrix pattern of up to about

30 non-identical nucleic acid molecules per square centimeter or higher, *e.g.* up to about 100 or even 1000 per square centimeter. Useful substrates for arrays include nylon, glass and silicon. *See*, for instance, US Patents 5,202,231; 5,445,934; 5,525,464; 5,700,637; 5,744,305; 5,800,992, the entirety of the disclosures of all of which are incorporated herein by reference. Sequences
5 can be efficiently analyzed by hybridization to a large set of oligonucleotides or cDNA molecules representing a large portion of a the genes of a genome. An array consisting of oligonucleotides or cDNA molecules complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be
10 screened with molecules or fragments thereof to determine nucleic acid molecules that specifically bind molecules or fragments thereof.

The microarray approach may also be used with polypeptide targets (U.S. Patent No. 5,445,934; U.S. Patent No:5,143,854; U.S. Patent No. 5,079,600; U.S. Patent No. 4,923,901, all of which are herein incorporated by reference in their entirety). Essentially, polypeptides are
15 synthesized on a substrate (microarray) and these polypeptides can be screened with either protein molecules or fragments thereof or nucleic acid molecules in order to screen for either protein molecules or fragments thereof or nucleic acid molecules that specifically bind the target polypeptides.

It is understood that one or more of the molecules of the present invention, preferably one
20 or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method. In a preferred embodiment of the present invention, one or more of the *E. nidulans* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method. A

particular preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that are homologs of known genes or nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is

5 a microarray comprising nucleic acid molecules having genes or fragments thereof that are homologs of known genes and nucleic acid molecules that comprise genes or fragment thereof that elicit only limited or no matches to known genes.

In a preferred embodiment, the microarray of the present invention comprises at least 10 nucleic acid molecules that specifically hybridize under high stringency to at least 10 nucleic acid molecules encoding *E. nidulans* protein or fragments. In a more preferred embodiment, the

10 microarray of the present invention comprises at least 100 nucleic acid molecules that specifically hybridize under high stringency to at least 100 nucleic acid molecules that encode an *E. nidulans* protein or fragment thereof. In an even more preferred embodiment, the microarray of the present invention comprises at least 1,000 nucleic acid molecules that specifically

15 hybridize under high stringency to at least 1,000 nucleic acid molecules that encode an *E. nidulans* protein or fragment thereof. In a further even more preferred embodiment, the microarray of the present invention comprises at least 2,500 nucleic acid molecules that specifically hybridize under high stringency to at least 2,500 nucleic acid molecules that encode an *E. nidulans* protein or fragment thereof. While it is understood that a single nucleic acid

20 molecule may encode more than one protein or fragment thereof, in a preferred embodiment, at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90% of the nucleic acid molecules that comprise the microarray encode one protein homolog or

fragment thereof. It is, of course, understood that these nucleic acid molecules can be non-identical.

In a preferred embodiment, the microarray of the present invention comprises at least 10 nucleic acid molecules that specifically hybridize under high stringency to at least 10 ENUs

5 selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either. In a more preferred embodiment, the microarray of the present invention comprises at least 100 nucleic acid molecules that specifically hybridize under high stringency to at least 100 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either. In an even more preferred

10 embodiment, the microarray of the present invention comprises at least 1,000 nucleic acid molecules that specifically hybridize under high stringency to at least 1,000 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either.. In a further even more preferred embodiment, the microarray of the present invention comprises at least 2,500 nucleic acid molecules that specifically hybridize under high stringency to at least 2,500 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either. While it is understood that a single nucleic acid molecule may encode more than one protein homolog or fragment thereof, in a preferred embodiment, at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90% of the nucleic acid molecules that comprise the

20 microarray encode one protein or fragment thereof.

Nucleic acid molecules of the present invention may be used in site directed mutagenesis. Site-directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be

altered (*e.g.* a threonine to be replaced by a methionine). Three basic methods for site-directed mutagenesis are often employed, *i.e.* (a) cassette mutagenesis, (b) primer extension and (c) methods based on PCR. *See* also US Patent 5,880,275, US Patent 5,380,831, and US Patent 5,625,136, the entirety of all of which is incorporated herein by reference.

5 Any of the nucleic acid molecules of the present invention may either be modified by site-directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners skilled in the art are familiar with such as isolating restriction fragments and ligating such fragments into an
10 expression vector.

Preferred aspects of this invention comprise collections of genes, nucleic acid molecules, polypeptides and/or primers of this invention ranging in size from about 10 non-identical members or more, *e.g.* at least about 100 or 270 or higher, more preferably at least about 300 or 350, most preferably at least 500 or higher, up to about 1000, or 2000 or even higher, say about
15 5000, or more non-identical members. As used herein a non-identical member is a member that differs in nucleic acid or amino acid sequence. For example, a non-identical nucleic acid molecule is a nucleic acid molecule that differs in nucleic acid sequence from the nucleic acid molecule to which it is being compared to. For example a nucleic acid molecule having the sequence 5' CCC 3' is not identical – *i.e.* non-identical – to a nucleic acid molecule having the
20 sequence 5' CCG 3'. In one aspect a collection may comprise all of the genes, nucleic acid molecules, polypeptides and/or primers of this invention. Such collections can be located or organized in a variety of forms, *e.g.* on microarrays, in solutions, in bacterial clone libraries, *etc.*

As used herein, an “organized” collection is a collection where the nucleic acid or amino acid sequence of a member of such a collection can be determined based on its physical location.

Preferred collections of nucleic acid molecules can be selected from the following groups: SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 26804 or complements thereof; SEQ ID NO: 26000 through SEQ ID NO: 26804 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 24035 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 22710 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 22709 or complements thereof; SEQ ID NO: 17681 through SEQ ID NO: 22709 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17680 or complements thereof; SEQ ID NO: 17618 through SEQ ID NO: 17680 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 17295 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17294 or complements thereof; SEQ ID NO: 28166 through SEQ ID NO: 44345 or complements thereof. Other preferred nucleic acid collections include any of the above groups but where such groups also include fragments of such sequences.

It is understood that all these preferred collections may also range in size from about 10 or more, *e.g.* at least about 100 or 270 or higher, more preferably at least about 300 or 350, most preferably at least 500 or higher, up to about 1000, or 2000 or even higher, say about 5000, or more non-identical members.

Another aspect of this invention provides the genes, nucleic acid molecules, polypeptides and/or primers in a substantially pure form. For instance, by use of the primers of this invention, any of the ENUs can be produced in substantially pure form by PCR.

Another aspect of this invention is to provide methods for determining gene expression, *e.g.* identifying homologous genes expressed by non-*E. nidulans* organism. Such methods comprise collecting mRNA from tissue of such organism, using the mRNA as a template for producing a quantity of labeled nucleic acid, and contacting the labeled nucleic acid molecule with a collection of purified nucleic acid molecules, *e.g.* on a microarray.

Computer Media

One or more of the nucleotide sequence provided in SEQ ID NO: 1, through SEQ ID NO: 44345 or complements or fragments of either can be “provided” in a variety of media to facilitate use. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences. In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, “computer readable media” refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; optical scanner readable medium such as printed paper; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST and/or BLAZE search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification, and DNA replication, restriction, modification, recombination, and repair.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or

implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 30 to 300 nucleotide residues or from about 10 to 100 of the corresponding amino acids. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, “a target structural motif,” or “target motif,” refers to any rationally selected sequence or combination of sequences in which the sequences the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above, and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various

amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

This example serves to illustrate the generation of the 16206 nucleic acid sequences listed in Table 1 as as contigs having SEQ ID NO: 1 through SEQ ID NO: 16206. About 390,000 genomic nucleotide sequence traces are derived from 11 different M13 and double stranded libraries. The two basic methods for the DNA sequencing are the chain termination method of Sanger *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 74:5463-5467 (1977) and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci. (U.S.A.)* 74:560-564 (1977) using automated fluorescence-based sequencing as reported by Craxton, *Method*, 2:20-26 (1991); Ju *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 92:4347-4351 (1995); and Tabor and Richardson, *Proc. Natl. Acad. Sci. (U.S.A.)* 92:6339-6343 (1995) and high speed capillary gel electrophoresis, *e.g.* as disclosed by Swerdlow and Gesteland, *Nucleic Acids Res.* 18:1415-1419 (1990); Smith, *Nature* 349:812-813 (1991); Luckey *et al.*, *Methods Enzymol.* 218:154-172 (1993); Lu *et al.*, *J. Chromatog. A.* 680:497-501 (1994); Carson *et al.*, *Anal. Chem.* 65:3219-3226 (1993); Huang *et al.*, *Anal. Chem.* 64:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis* 17:1852-1859 (1996); Quesada and Zhang, *Electrophoresis* 17:1841-1851 (1996); Baba, *Yakugaku Zasshi* 117:265-281 (1997). For instance, genomic nucleotide sequence traces are generated using a 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allowing for rapid electrophoresis and data collection. With these types of automated systems, fluorescent dye-

labeled sequence reaction products are detected and chromatograms are subsequently viewed, stored in computer and analyzed using corresponding apparatus-related software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, Cold Spring Harbor, New York.

5 Over 390,000 quality genomic sequence traces are assembled generally as follows:

- (a) all traces are quality clipped using *yc_qual_clip.pl* (with a minimum PHRED score of 12.5 and maximum length of 50 bp);
- (b) all traces are segregated according to library construction method;
- (c) all traces are “vector-trimmed” *i.e.*, 5’ and 3’ vector and linker sequences are
10 removed;
- (d) all traces are re-united in one file;
- (e) all traces are then clustered with PANGAEA’s clustering tool (available from Pangea Corp., Pittsburgh, PA). A cluster includes 2 or more traces of sequences with 90% similarity over 60 bp. After clustering the set of traces includes clusters and
15 non-clustered traces referred to as “singletons”.
- (f) A high stringency PHRAP assembly is run on each cluster to separate from clusters singlet traces which do not meet stringency criteria. The arguments to high stringency PHRAP are: minmatch 25 , minscore 50, penalty -4 ;
- (g) Contigs and the singleton (including singlet) traces and their corresponding
20 quality files are united; and, then are assembled with a low stringency PHRAP (using default PHRAP arguments) to generate a “final” assembly; and
- (h) the final set of 16,144 nucleic acid sequences (identified in Table 1 by contig identification number “ANI61xxxx” and by the corresponding SEQ ID NO: 1 through

SEQ ID NO:16144) and 52 nucleic acid sequences (identified in Table 1 by contig identification number "ANI50xxxx" and by corresponding SEQ ID NO: 16145 through SEQ ID NO:16206) are run through the annotation and gene selection processes. Contigs in SEQ ID NO:1 through SEQ ID NO:16144 are recognized as those sequences whose designations begin with ANI61C or ANI50C. Singleton sequences are recognized as those having designations which begin with ANI61S or ANI50S.

The genomic sequence traces and many of the contigs and singleton traces are disclosed in copending provisional applications for patent identified by serial nos. 60/ 101,665; 60/101,666; 60/102,358; 60/113,361; 60/126,265; 60/130,189; 60/130,190; 60/132,861; 60/138,103; 60/149,882.

Example 2

This example illustrates the identification of ENUs within 16206 contigs assembled in Example 1. The genes and partial genes embedded in such contigs are identified through a series of informatic analyses. The tools to define genes fall into two categories: homology-based and predictive-based methods. Homology-based searches (*e.g.*, GAP2, NAP, BLASTX and TBLASTX) detect conserved sequences during comparisons of DNA sequences or hypothetically translated protein sequences to public and/or proprietary DNA and protein databases. Existence of a *E. nidulans* gene is inferred if significant sequence similarity extends over the majority of the target gene. Since homology-based methods may overlook genes unique to *E. nidulans*, for which homologous nucleic acid molecules have not yet been identified in databases, gene prediction programs are also used. Predictive methods employed in the definition of the *E. nidulans* genes included the use of the GenScan gene predictive software

program which is available from Stanford University (e.g. at the web site

<http://gnomic.stanford.edu/GENSCANW.html>). GenScan, in general terms, infers the presence and extent of a gene through a search for “gene-like” grammar.

The homology-based methods used to define the *E. nidulans* gene set included GAP2,

5 BLASTX supplemented by NAP, and TBLASTX. For a description of BLASTX and

TBLASTX see Coulson, *Trends in Biotechnology* 12:76-80 (1994) and Birren *et al.*, *Genome*

Analysis, 1:543-559 (1997). GAP2 and NAP are part of the Analysis and Annotation Tool (AAT)

for Finding Genes in Genomic Sequences which was developed by Xiaoqiu Huang at Michigan

Tech University and is available at the web site <http://genome.cs.mtu.edu/>. The AAT package

10 includes two sets of programs, one set (DPS/NAP) for comparing the query sequence with a protein database, and the other set (DDS/GAP2) for comparing the query sequence with a cDNA database. Each set contains a fast database search program and a rigorous alignment program.

The database search program quickly identifies regions of the query sequence that are similar to a

database sequence. Then the alignment program constructs an optimal alignment for each region

15 and the database sequence. The alignment program also reports the coordinates of exons in the query sequence. See Huang, *et al.*, *Genomics* 46: 37-45 (1997).

The GAP2 program computes an optimal global alignment of a genomic sequence and a cDNA sequence without penalizing terminal gaps. A long gap in the cDNA sequence is given a constant penalty. The DNA-DNA alignment by GAP2 adjusts penalties to accommodate introns.

20 The GAP2 program makes use of splice site consensus in alignment computation. GAP2

delivers the alignment in linear space, so long sequences can be aligned. See Huang, *Computer*

Applications in the Biosciences 10 227-235 (1994). The GAP2 program aligned the *E. nidulans*

contigs with the *A. nidulans*/*E. nidulans* EST library in the microorganism databank maintained by Bruce Roe's laboratory at the University of Oklahoma.

The NAP program computes a global alignment of a DNA sequence and a protein sequence without penalizing terminal gaps. NAP handles frameshifts and long introns in the DNA sequence. The program delivers the alignment in linear space, so long sequences can be aligned. It makes use of splice site consensus in alignment computation. Both strands of the DNA sequence are compared with the protein sequence and one of the two alignments with the larger score is reported. See Huang, and Zhang, "Computer Applications in the Biosciences" 12(6), 497-506 (1996).

NAP takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database (e.g. the non-redundant protein (i.e., nr-aa) database maintained by the National Center for Biotechnology Information as part of GenBank and available at the web site: <http://www.ncbi.nlm.nih.gov>). TBLASTX compared six possible frame translations of the *E. nidulans* contigs against six frame translations of *Aspergillus fumigatus*, *Fusarium graminearum*, *Saccharomyces cerevisiae*, and *Candida albicans* genomic sequences.

The first homology-based search for genes in the *E. nidulans* contigs is effected using the GAP2 program and the University of Oklahoma *A. nidulans*/*E. nidulans* EST database. A collection of about 14000 *A. nidulans*/*E. nidulans* EST sequences from the database with known 5' and 3' orientations and mate information are clustered into about 3500 distinct sets or "clusters". These clusters are then mapped onto an assembly of *E. nidulans* contigs represented by SEQ ID NO. 1 through SEQ ID NO. 16206 using the GAP2 program. GAP2 standards for selecting a DNA-DNA match were $\geq 96\%$ sequence identity with the following parameters:

gap extension penalty = 1

match score = 2

gap open penalty = 6

gap length for constant penalty = 20

5 mismatch penalty = -2

minimum exon length = 21

DNA matches with ESTs fell into three categories. Firstly, ENUs are identified when a 5'-3' EST pair aligned to the sequences on the same contig. Since EST's are necessarily derived from genes, no corroborating evidence is required to validate the gene prediction. Certain ENUs are identified by 5'-3' EST pair match on a single contig. These ENUs are identified by "EST" in the selection basis column of Table 2 and include SEQ ID NO. 16207 through SEQ ID NO. 17294.

Another group of ENUs identified by DNA match with EST's is selected because of alignment of a 5'-3' EST pair which spanned two contigs supported by BLASTX similarity or clonemate information. These ENUs are identified by "MCEST" in the selection basis column of Table 2 and include SEQ ID NO. 17618 through SEQ ID NO. 17680.

Another group of ENUs identified by DNA match with EST's is selected solely from a 3' EST match of at least 300 bp using EST's which are not previously aligned. These ENUs are identified by "TPEST" in the selection basis column of Table 2 and include SEQ ID NO. 17295 through SEQ IS NO. 17617.

The second homology-based method used for gene discovery is BLASTX hits extended with the NAP software package. BLASTX is run with the *E. nidulans* contigs represented by SEQ ID NO. 1 through SEQ ID NO. 16206 as queries against the GenBank non-redundant

protein data library identified as “nr-aa”. NAP is used to better align the amino acid sequences as compared to the genomic sequence. NAP extends the match in regions where BLASTX has identified high-scoring-pairs (HSPs), predicts introns, and then links the exons into a single ORF prediction. Experience suggests that NAP tends to mis-predict the first exon. *E. nidulans* introns

are almost without exception short (<150 bp), and NAP routinely predicts very long (>400 bp) introns leading to a very short, and biologically unmeaningful, 5' exon. The NAP-predicted ORFs containing long introns (>175 bp) are first segregated and truncated (the long intron and the nonsense 5' exon removed) and the remaining portion of the ORF established as a gene.

Selection in a first pass is for sequences with (a) <600 bp from the 3' end with >50% coverage,

(b) <600 bp from the 3' end with > 300 bp coverage and (c) >1000 bp from the 3' end with 500 bp coverage. Selection in a second pass is for sequences with (a) <300 bp from the 3' end with ,500 bp coverage and >80% coverage or (b) <300 bp from the 3' end and > 500 bp coverage.

The NAP parameters are:

gap extension penalty = 1

gap open penalty = 15

gap length for constant penalty = 25

min exon length (in aa) = 7

The ENUs identified by NAP with (a) >300 bp and >10% homology or (b) >175 bp and > 50% coverage are identified by “NAP” in the selection basis column of Table 2 and include SEQ ID NO. 17681 through SEQ ID NO. 22709.

For NAP alignments with large introns GenScan are used to locate the terminal exon and extend the 5' end of the terminal exon. When there is no GenScan indication of a terminal exon,

the gene is identified using the longest exon cluster without a large intron. The ENUs identified from large intron alignments are identified by “LINAP” in the selection basis column of Table 2 and include SEQ ID NO. 22710 through SEQ ID NO. 24034.

In the final homology-based method, TBLASTX, is used with genome information from three fungal genome sequencing projects: *Aspergillus fumigatus*, *Fusarium graminearum*, *Saccharomyces cerevisiae* and *Candida albicans*. As a general rule, non-coding regions of DNA accumulate mutations much more rapidly than coding regions. With this knowledge, we use TBLASTX, which compares hypothetical translations, to identify regions of DNA that code for highly similar amino acid strings in both *E. nidulans* and the four other fungal genomes. As with EST matches, the TBLASTX hits fall into three categories of defined genes: matches that fall within an *E. nidulans* contig, matches that convincingly bridge contigs, and long matches that contain sufficient portions of a gene for use in transcriptional profiling. Unlike GAP2 and BLASTX/NAP analyses, we have comparatively little experience in interpreting TBLASTX scores as a tool for defining the unigene set. For this reason, conservative standards for inclusion of TBLASTX hits into the gene set are utilized. These standards are a minimal E value of 1E-20, and for terminal exons, a minimal match of 200 bp within the 1000 most 5' and 3' ends of an *E. nidulans* contig. In addition to these criteria, in part due to conflicting data from TBLASTX analyses (where different TBLASTX matches will suggest two or more mutually exclusive possibilities) and to concerns that repeat regions may be sufficiently similar to confound the method, TBLASTX predicted genes bridging two contigs are included when corroborating evidence in the form of GenScan predictions and/or clone mate evidence from double stranded clones is available.

The GenScan program is “trained” with *E. nidulans* characteristics. Though better than the “off-the-shelf” version, the GenScan trained to identify *E. nidulans* genes proved more proficient at predicting exons than predicting full-length genes. Predicting full-length genes is compromised by point mutations in the unfinished contigs, as well as by the short length of the contigs relative to the typical length of a gene. Due to the errors found in the full-length gene predictions by GenScan, inclusion of GenScan-predicted genes is limited to those genes and exons whose probabilities are above a conservative probability threshold. When used with TBLASTX the GenScan parameters are:

- mean GenScan P value > 0.3
- mean GenScan T value > 0
- mean GenScan Coding score > 50
- length > 200 bp
- minimum TBLASTX E value < 1E-20

Significant TBLASTX hits to single contigs that are greater than 300 bp contributed 805 genes to the unigene set. The high E value threshold limited the vast majority (99%) of the TBLASTX hits to the fungal genome comparisons. The TBLASTX hits with GenScan corroboration identified 1965 ENUs identified by “GTBX” in the selection basis column of Table 2 and include SEQ ID NO. 24035 through SEQ ID NO. 25999.

To identify ENUs solely by TBLASTX, the TBLASTX E values is set at 1E-30 with a length of > 200 bp. The ENU’s identified solely by TBLASTX are identified by “TBX” in the selection basis column of Table 2 and include SEQ ID NO. 26000 through SEQ ID NO. 26804.

A final set of genes is predicted using the GenScan program “trained” with *E. nidulans* characteristics and the mean GenScan P value parameters changed to > 0.4. The ENUs identified

solely by GenScan are identified by “GSP” in the selection basis column of Table 2 and include SEQ ID NO. 26805 through SEQ ID NO. 27905.

To insure that the same nucleic acid molecule is not inferred two or more times with different methods, an all-versus-all BLASTN analysis of the all the identified ENUs is conducted. There are instances where sequencing and assembly errors will confound the identification of duplicates, but such instances are comparatively rare.

The confidence in accuracy of the identified ENUs is highest for those identified by a match of a 5'-3' EST to a single contig (identified by EST) and lowest for those identified solely the GenScan predictive algorithm (identified by GSP). The order of confidence for the ENUs is in the following order:

<u>Selection Basis</u>	<u>Confidence</u>
EST	highest
TPEST	
MCEST	
NAP	
LINAP	
GTBX	
TBX	
GSP	lowest

In Table 2 the ENUs of this invention are identified in the sequence identification (seq. id.) column the name ENU (*Emericella nidulans* unigene) and begins with ENU00001 for SEQ ID NO. 16207.

Other modifications of the above described embodiments of the invention which are obvious to those of skill in the area of molecular biology and related disciplines are intended to be within the scope of the following claims.

Example 3

This example serves to illustrate the design of primers of this invention which are useful, for instance, for initiating synthesis of nucleic acid molecules of this invention, specifically substantial parts of certain ENU's of this invention. The primers specifically disclosed herein, *i.e.* in Table 3 by SEQ ID NO. 28166 through SEQ ID NO. 44345, are designed with the program Primer3 (obtained from the MIT-Whitehead Genome Center) with a "perl-oracle" wrapper. The criteria applied to design a primer included:

Primer annealing temperature (minimum 65°C, optimum 70°C, maximum 75 °C)

Primer length (minimum 18bp, optimum 20bp, maximum 28 bp)

G+C content (minimum 20%, maximum 80%)

Position of the primer relative to the gene

Length of the amplified region (500 to 800 bp)

PHRED quality score of the gene template (minimum of 20)

Whether the gene was defined from one or two contigs

Maximum mismatch = 12.0 (weighted score from Primer3 program)

Pair Max Misprime = 24.0 (weighted score from Primer3 program)

Maximum N's = 0

Maximum poly-X = 5

The primary goal of the design process is the creation of groups of primer pairs with a common annealing temperature (T_m). When the program could identify a primer pair for any gene that fit the criteria, the gene is removed from the bin of genes needing primer design. Genes remaining in the bin are subjected to additional rounds of primer-picking, with the gradual and simultaneous relaxation of the criteria (*i.e.*, lowering the annealing temperature, increasing

the size of the window where primers could be predicted, expanding the range of permitted size and G+C content, removing the need for a G/C clamp), until primers are picked for about 8,000 of the about 12,000 ENUs of this invention. After the *E. nidulans* specific portion of the primers is selected, an additional common primer tail sequence (universal primer) is added to the 5' ends.

5 For the forward primers, the additional common bases added are:

(5'-GAATTCAGTGGCGCCGCGCATG-3'); for the reverse primers the additional common bases added are: (5'-GTTCTCGAGACGAGCGATCGC-3'). The universal primer tail sequences are added so that subsequent reamplifications of any primer pair can be done with a single set of primers. In addition, the primer tail sequences contain restriction digestion sites for
 10 8 bp cutters (NotI and SgfI) and 6 bp cutters (EcoRI and XhoI) to facilitate cloning of ENUs into vectors. The forward primers contains EcoRI and NotI restriction sites; the reverse primers contains XhoI and SgfI restriction sites.

Reference is also made to Tables 2 and 3 for identification of the primers and reference to the ENU for which they are designed. The primer pair for a particular ENU is identified in Table
 15 2 by indication of the complementary or identical nucleotides in the particular ENU under the columns "Primer 5 pos" and "Primer 3 pos". The primer sequence numbers in Table 3 correspond to an ENU identified in the "Seq id" column. For example, the primer pair ENU00001p5 and ENU00001p3 represent the sequences for the 5' and 3' primer, respectively for ENU00001. The primer sequences provided in the sequence listing all contain the universal
 20 tail sequence described above as the first 21 nucleotides. It is noted that primer pairs are not required to contain the universal tail sequence, the relevant portion for amplification and/or hybridization probes being the *E. nidulans* specific sequences designated in the "Primer 5 pos" and "Primer 3 pos" columns in Table 2.

Table 1

Seq num	Contig_id
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16150	ANI50C12827_1
16151	ANI50C14154_1
16152	ANI50C14692_1
16153	ANI50C16799_1
16154	ANI50C17436_1
16155	ANI50C1823_6
16156	ANI50C1851_1
16157	ANI50C1_1010
16158	ANI50C1_1035
16159	ANI50C1_1118
16160	ANI50C1_1662
16161	ANI50C1_1680
16162	ANI50C1_1741
16163	ANI50C1_1781
16164	ANI50C1_1901
16165	ANI50C1_1904
16166	ANI50C1_243
16167	ANI50C20068_1
16168	ANI50C202_3
16169	ANI50C21776_1
16170	ANI50C23500_1
16171	ANI50C236901_1
16172	ANI50C24497_1
16173	ANI50C27389_1
16174	ANI50C2734_1
16175	ANI50C30369_2
16145	ANI50C346_1
16176	ANI50C34975_1
16177	ANI50C36650_1
16178	ANI50C392_1
16179	ANI50C392_2
16180	ANI50C4357_1

Table 2

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16207	ENU00001	ANI61C5803: 2968..3252	38-57	261-280	EST	"3h09a1.r1, 13h09a1.fl"			32	1			probable 60S ribosomal protein C2E11.04 ; (AL031181) 60s ribosomal protein L28 [Schizosaccharomyces pombe] ; (AL035064) 60s ribosomal protein l28 [Schizosaccharomyces pombe]
16208	ENU00002	ANI61C4566: 5066..5474	40-59	375-406	EST	"y6a02a1.r1, y6a02a1.fl"			33	1.1			(AL021841) PE_PGERS [Mycobacterium tuberculosis] (AF130355) Pad-1 [Neurospora crassa]
16209	ENU00003	ANI61C486:1 033..8	86-113	1034-1069	EST	"c9d02a1.r1, c9d02a1.fl"			269	2E-71			(U31653) particulate methane monooxygenase [Methylomonas methanica]
16210	ENU00004	ANI61C7400: 91..607	112-131	560-585	EST	"w4b01a1.r1, w4b01a1.fl"			32	3.6			(Z95397) unknown [Schizosaccharomyces pombe] (AL031786) hypothetical protein. [Schizosaccharomyces pombe] (AE001251) exoribonuclease II (rmb) [Treponema pallidum]
16211	ENU00005	ANI61C5660: 106..672	110-128	613-634	EST	"o9f10a1.r1, o9f10a1.fl"			56	0.000000			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16212	ENU00006	ANI61C1405: 3433..3638	120-139	259-283	EST	"w4c07a1.r1, w4c07a1.fl"			63	2E-10			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16213	ENU00007	ANI61C9317: 4348..4148	40-59	720-740	EST	"c5c05a1.r1, c5c05a1.fl"			33	2			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16214	ENU00008	ANI61C9324: 54..253	38-59	171-195	EST	"d5e06a1.r1, d5e06a1.fl"			30	2.5			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16215	ENU00009	ANI61C9324: 61..260	45-64	180-202	EST	"c8f05a1.r1, c8f05a1.fl"			29	3.3			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16216	ENU00010	ANI61C9324: 54..253	38-59	171-195	EST	"l0g12a1.r1, l0g12a1.fl"			30	2.5			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16217	ENU00011	ANI61C9324: 41..240	25-48	159-182	EST	"y6b07a1.r1, y6b07a1.fl"			30	2.5			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16218	ENU00012	ANI61C4812: 437..636	44-63	182-201	EST	"z3d11a1.r1, z3d11a1.fl"			143	1E-34			(D87063) chitinase [Emericella nidulans]
16219	ENU00013	ANI61C9324: 54..253	38-59	171-195	EST	"z4a05a1.r1, z4a05a1.fl"			30	2.5			prostaglandin transporter (PGT) (matrin F/G) ; prostaglandin transporter - rat
16220	ENU00014	ANI61C4718: 1244..1453	38-57	186-205	EST	"y3h12a1.r1, y3h12a1.fl"			32	0.5			ubiquitin 1 - Tetrahymena pyriformis (SGC5) (fragment) ; (M24081) ubiquitin [Tetrahymena pyriformis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16221	ENU00015	ANI61C4718: 1244..1453	38-57	186-205	EST	"g3c04a1.rl, g3c04a1.fl"			32	0.5			ubiquitin 1 - Tetrahymena pyriformis (SGC5) (fragment) ; (M24081) ubiquitin [Tetrahymena pyriformis] (D87063) chitinase [Emerticella nidulans] (D87063) chitinase [Emerticella nidulans] translational activator GCN1 ; translation activator GCN1 - yeast (Saccharomyces cerevisiae) ; (L12467) translational activator [Saccharomyces cerevisiae] ; (X91837) translational activator GCN1 [Saccharomyces cerevisiae] ; (Z72717) ORF YGL195w [Saccharomyces cerevisiae] phospholipase A2 (EC 3.1.1.4) precursor - Chinese habu "asparaginyl-TRNA synthetase, mitochondrial precursor (asparagine--TRNA ligase) (ASNRS) ; hypothetical protein YCR024c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR024c, len:492 [Saccharomyces cerevisiae] "
16222	ENU00016	ANI61C4812: 414..625	22-42	172-191	EST	"r1d06a1.rl, r1d06a1.fl"			154	9E-38			
16223	ENU00017	ANI61C4812: 414..625	22-42	172-191	EST	"r1b07a1.rl, r1b07a1.fl"			154	9E-38			
16224	ENU00018	ANI61C6468: 2109..1879	70-89	240-258	EST	"z4g03a1.rl, z4g03a1.fl"			31	1.9			
16225	ENU00019	ANI61C3987: 1271..1504	61-80	233-252	EST	"r4e03a1.rl, r4e03a1.fl"			32	0.66			
16226	ENU00020	ANI61C7278: 2805..3039	64-83	236-256	EST	"j0a09a1.rl, j0a09a1.fl"			28	9.8			
16227	ENU00021	ANI61S3058: 312..50	24-42	225-244	EST	"n8d06a1.rl, n8d06a1.fl"			151	9E-37			"60S ribosomal protein L13A (RP22) ; ribosomal protein L16.e.A, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 199, CAl: 0.62, predicted to be spliced, similar to A44367 A44367 P23=tumor-specific transplantation antigen and ribosomal proteins [Saccharomyces cerevisiae] "
16228	ENU00022	ANI61C6046: 484..171	28-47	278-299	EST	"c1b10a1.rl, c1b10a1.fl"			29	8.4			Apical endosomal glycoprotein precursor ; apical endosomal protein precursor - rat ; (L37380) apical endosomal glycoprotein [Rattus norvegicus] (AJ131708) gamma response I protein [Arabidopsis thaliana]
16229	ENU00023	ANI61C1658: 1936..2297	55-74	355-374	EST	"r7d05a1.rl, r7d05a1.fl"			31	4.8			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16230	ENU00024	ANI61C584:8 20..1208	56-75	382-401	EST	"y8g11a1.r1, y8g11a1.fl"			131	2E-30			nucleoside diphosphate kinase (NDK) (NDP kinase); nucleoside-diphosphate kinase (EC 2.7.4.6) - yeast (Saccharomyces cerevisiae); (X75780) A153 [Saccharomyces cerevisiae]; (D13562) nucleoside diphosphate kinase [Saccharomyces cerevisiae]; (Z28067) ORF YKL067w [Saccharomyces cerevisiae]; nucleoside diphosphate kinase [Saccharomyces cerevisiae] protein-glutamine glutamyltransferase E3 precursor (TGase E3) (transglutaminase 3); (L10385) transglutaminase E3 [Mus musculus] (L36960) glycerol-3-phosphate dehydrogenase [Ceratitis capitata]
16231	ENU00025	ANI61C137:3 810..4223	70-89	415-441	EST	"10b10a1.r1, 10b10a1.fl"			31	5.9			hypothetical 93.9 KD protein T20B12.6 in chromosome III; (U10401) T20B12.6 gene product [Caenorhabditis elegans] hydroxyproline-rich glycoprotein (clone Hyp2.13) - kidney bean (fragment); (M18095) hydroxyproline-rich glycoprotein [Phaseolus vulgaris] (AJ002531) nosL [Bradyrhizobium japonicum] (AF093142) aconitase [Aspergillus terreus] (U88184) F36H5.3 gene product [Caenorhabditis elegans] (Z99112) similar to hypothetical proteins [Bacillus subtilis] (AJ002291) penicillin-binding protein 1b [Streptococcus pneumoniae]
16232	ENU00026	ANI50S1275: 466..39	26-45	389-411	EST	"t2e03a1.r1, t2e03a1.fl"			76	9E-14			
16233	ENU00027	ANI61C6109: 2589..2139	61-80	445-469	EST	"o8d08a1.r1, o8d08a1.fl"			50	0.000008			
16234	ENU00028	ANI61C7998: 3381..3855	32-51	447-464	EST	"z4g12a1.r1, z4g12a1.fl"			43	0.001			
16235	ENU00029	ANI61C412:2 192..2691	59-78	497-516	EST	"c8c12a1.r1, c8c12a1.fl"			32	3.3			
16236	ENU00030	ANI61C9735: 6052..6639	23-42	548-568	EST	"i2c01a1.r1, i2c01a1.fl"			157	1E-38			
16237	ENU00031	ANI61C1708: 1586..2176	61-78	589-609	EST	"m5c06a1.r1, m5c06a1.fl"			33	2.2			
16238	ENU00032	ANI61C1110 4:2085..1446	71-90	634-668	EST	"i8g03a1.r1, i8g03a1.fl"			36	0.25			
16239	ENU00033	ANI61C5131: 985..335	60-80	649-668	EST	"j4e04a1.r1, j4e04a1.fl"			34	1.3			
16240	ENU00034	ANI61C4335: 86..752	55-76	660-679	EST	"m0h05a1.r1, m0h05a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16248	ENU00042	ANI61C5969: 106..1208	25-44	1066-1085	EST	"w6b10a1.rl", w6b10a1.fl"			37	0.22			"Glutenin, high molecular weight subunit PW212 precursor ; glutenin, high molecular weight chain precursor - wheat ; (X03346) glutenin [Triticum aestivum] "
16249	ENU00043	ANI61C1087: 482..678	41-62	1317-1351	EST	"r7f11a1.rl", r7f11a1.fl"		122		7E-27			(U81790) PIG8 [Uromyces fabae]
16250	ENU00044	ANI61C7027: 1396..15	46-65	1365-1385	EST	"w8c04a1.rl", w8c04a1.fl"		490		e-138			Carboxypeptidase Y precursor (carboxypeptidase YSCY) (AF080683) PITSLRE protein kinase alpha SV5 isoform [Homo sapiens]
16251	ENU00045	ANI61C8717: 4377..2914	25-44	1425-1445	EST	"m2h12a1.rl", m2h12a1.fl"		42		0.012			putative iron alcohol dehydrogenase ; probable alcohol dehydrogenase (EC 1.1.1.1) - fission yeast
16252	ENU00046	ANI61C4015: 1137..938	26-47	149-183	EST	"j4f02a1.rl", j4f02a1.fl"		29		4.4			(Schizosaccharomyces pombe) ; (Z49811) iron containing alcohol dehydrogenase [Schizosaccharomyces pombe]
16253	ENU00047	ANI61C3597: 1117..924	46-64	186-203	EST	"d5b05a1.rl", d5b05a1.fl"		31		0.86			(Z95150) hypothetical protein Rv3127 [Mycobacterium tuberculosis]
16254	ENU00048	ANI61C8436: 715..921	35-54	170-199	EST	"p0h09a1.rl", p0h09a1.fl"		29		4.3			(Z81050) Similarity to C.elegans ligand-gated ion channels [Caenorhabditis elegans]
16255	ENU00049	ANI61C6647: 4466..4249	67-86	220-243	EST	"h4c04a1.rl", h4c04a1.fl"		30		1.9			(U63336) MHC Class I region proline rich protein [Homo sapiens]
16256	ENU00050	ANI61C8167: 1190..961	62-84	216-249	EST	"r7e12a1.rl", r7e12a1.fl"		36		0.056			(Z99295) citrate lyase [Schizosaccharomyces pombe]
16257	ENU00051	ANI61C9308: 786..997	38-59	214-233	EST	"e9c05a1.rl", e9c05a1.fl"		35		0.1			nucleic acid-binding protein E5.1 - human ; (L37368) RNA-binding protein [Homo sapiens]
16258	ENU00052	ANI61C2422: 1029..1270	32-53	204-231	EST	"j9f12a1.rl", j9f12a1.fl"		29		6.3			(AE001279) hypothetical protein [Chlamydia trachomatis]
16259	ENU00053	ANI61C6468: 1816..2056	26-47	196-229	EST	"w9f11a1.rl", w9f11a1.fl"		29		6.6			(U89708) unknown [Leptospira interrogans serovar lai]
16260	ENU00054	ANI61C6468: 2170..1924	25-48	207-229	EST	"z4g06a1.rl", z4g06a1.fl"							(X85254) polymerase [Hepatitis B virus]
16261	ENU00055	ANI61C1061: 1698..1953	65-86	248-278	EST	"z5f07a1.rl", z5f07a1.fl"		29		7.2			(U65409) Sla2p [Yarrowia lipolytica]
16262	ENU00056	ANI61C3434: 2506..2249	22-55	208-237	EST	"c6c12a1.rl", c6c12a1.fl"		38		0.019			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16263	ENU00057	ANI61C2786: 52-75 381..121	52-75	240-270	EST	"y3g09a1.r1, y3g09a1.fl"			31	1.5		(AL023635) hypothetical protein MLCB1243.36 [Mycobacterium leprae]
16264	ENU00058	ANI61C4718: 45-66 1697..1183	45-66	261-296	EST	"w7a05a1.r1, w7a05a1.fl"		46		0.00009		ubiquitin S2 [Drosophila melanogaster]
16265	ENU00059	ANI61C1794: 22-47 3511..3217	22-47	239-274	EST	"s8f04a1.r1, s8f04a1.fl"		97		3E-20		(AB007770) translation elongation factor 1 alpha [Aspergillus oryzae]
16266	ENU00060	ANI61C4718: 42-61 2247..1211	42-61	261-296	EST	"i8h04a1.r1, i8h04a1.fl"		69		1E-11		(X08013) ubiquitin (752 is 2nd base in codon) [Cricetulus sp.]
16267	ENU00061	ANI61C4718: 42-61 2247..1211	42-61	261-296	EST	"q0g06a1.r1, q0g06a1.fl"		69		1E-11		(X08013) ubiquitin (752 is 2nd base in codon) [Cricetulus sp.]
16268	ENU00062	ANI61C4718: 42-61 2247..1211	42-61	261-296	EST	"f1d09a1.r1, f1d09a1.fl"		69		1E-11		(X08013) ubiquitin (752 is 2nd base in codon) [Cricetulus sp.]
16269	ENU00063	ANI61C4718: 22-41 2247..1208	22-41	244-279	EST	"a0f02a1.r1, a0f02a1.fl"		69		1E-11		(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
16270	ENU00064	ANI61C4718: 42-61 2247..1208	42-61	264-299	EST	"r4e11a1.r1, r4e11a1.fl"		69		1E-11		(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
16271	ENU00065	ANI61C8760: 45-64 272..574	45-64	268-303	EST	"q0e09a1.r1, q0e09a1.fl"		41		0.000000		(AJ001272) manganese resistance 1 protein [Saccharomyces cerevisiae]
16272	ENU00066	ANI61C1010 30-53 1:2112..1798	30-53	283-303	EST	"o6g04a1.r1, o6g04a1.fl"		31		3.1		"DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa] ; phosphoprotein ARPP-32 [Homo sapiens]"
16273	ENU00067	ANI61C1147 22-52 7:3288..3617	22-52	286-309	EST	"w4a04a1.r1, w4a04a1.fl"						hypothetical protein o259a - Escherichia coli ; (U14003)
16274	ENU00068	ANI61C1368: 29-48 737..1068	29-48	294-318	EST	"d3f05a1.r1, d3f05a1.fl"		31		3.1		ORF_o259a [Escherichia coli] ; (AE000492) FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli]
16275	ENU00069	ANI61C5614: 22-54 150..486	22-54	288-316	EST	"z3d01a1.r1, z3d01a1.fl"		36		0.12		(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]
16276	ENU00070	ANI61C2246: 39-58 20..357	39-58	311-334	EST	"t2c05a1.r1, t2c05a1.fl"		183		3E-46		(AF035434) elongation factor 3 [Aspergillus fumigatus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16277	ENU00071	ANI61C2013: 35-66 476..820	35-66	302-337	EST	"w4a02a1.r1, w4a02a1.fl"			36	0.099			(AL031852) putative metal homeostasis factor [Schizosaccharomyces pombe]
16278	ENU00072	ANI61C7988: 66-85 1302..1651	66-85	348-373	EST	"z4f05a1.r1, z4f05a1.fl"		127		4E-35			putative proteasome component C9/Y13 (macropain subunit) (multicatalytic endopeptidase complex subunit); hypothetical protein SPA13C5.01c - fission yeast (Schizosaccharomyces pombe); (Z50112) proteosome A- type subunit [Schizosaccharomyces pombe]
16279	ENU00073	ANI61S1034: 48-67 45..401	48-67	343-362	EST	"z2b09a1.r1, z2b09a1.fl"		40		0.007			(D83992) similar to gpi: SCU43281_10 Lpg10p (56.7% identity in 60 aa overlap) [Schizosaccharomyces pombe]
16280	ENU00074	ANI50S2543: 54-73 37..408	54-73	363-383	EST	"y8h12a1.r1, y8h12a1.fl"		30		0.28			ribosomal protein L37a; 60S ribosomal protein L37A; ribosomal protein L37a - rat; ribosomal protein L37a - human; ribosomal protein L37a - mouse; (X66699) ribosomal protein L37a [Homo sapiens]; (X14069) ribosomal protein L37a (AA 1 - 92) [Rattus rattus]; (L06499) ribosomal protein L37a [Homo sapiens]; (X73331) ribosomal protein L37a [Mus musculus]
16281	ENU00075	ANI61C5524: 22-47 1660..1284	22-47	321-356	EST	"y4f05a1.r1, y4f05a1.fl"		46		0.000000 001			40S ribosomal protein S14 (CRP2); (X53734) ribosomal protein crp-2 [Neurospora crassa]
16282	ENU00076	ANI61S2489: 22-55 12..391	22-55	327-359	EST	"m8c07a1.r1, m8c07a1.fl"		31		3			(AF002222) PvcB [Pseudomonas aeruginosa]
16283	ENU00077	ANI61C7366: 61-80 1189..818	61-80	373-398	EST	"t2g04a1.r1, t2g04a1.fl"		34		0.46			putative reverse transcriptase [Arabidopsis thaliana]
16284	ENU00078	ANI61C8333: 29-50 1658..1278	29-50	339-368	EST	"l0h12a1.r1, l0h12a1.fl"		66		8E-11			(U95045) velvet A [Emericella nidulans]
16285	ENU00079	ANI61C3987: 22-49 947..559	22-49	344-368	EST	"f2h12a1.r1, f2h12a1.fl"		32		1.8			(AF007193) mucin [Homo sapiens]
16286	ENU00080	ANI61C1031: 24-46 7:492..102	24-46	338-371	EST	"z4a10a1.r1, z4a10a1.fl"		54		0.000000 4			hypothetical protein YDR313c - yeast (Saccharomyces cerevisiae); (U28374) YDR313C gene product [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16287	ENU00081	ANI61C1069 1:2879..3271	69-88	400-419	EST	"x7d07a1.r1, x7d07a1.fl"			183	5E-46			signal recognition particle 54 KD protein homolog ; signal recognition particle 54K protein homolog - Aspergillus niger ; (L38317) srpA gene product [Aspergillus niger] ; srpA gene [Aspergillus niger]
16288	ENU00082	ANI61C1067 4:424..30	62-82	393-414	EST	"i0a04a1.r1, i0a04a1.fl"			55	0.000000 2			(AL031966) hypothetical HIT-family protein [Schizosaccharomyces pombe]
16289	ENU00083	ANI61C1067 4:424..30	62-82	393-414	EST	"t2d07a1.r1, t2d07a1.fl"			55	0.000000 2			(AL031966) hypothetical HIT-family protein [Schizosaccharomyces pombe]
16290	ENU00084	ANI61C1053 6:482..86	49-68	384-403	EST	"y8f11a1.r1, y8f11a1.fl"			31	5.5			(X82877) sodium-D-glucose cotransporter [Homo sapiens]
16291	ENU00085	ANI61C3270: 208..604	22-44	357-376	EST	"x5g08a1.r1, x5g08a1.fl"			31	5.5			(D84678) omega-3 fatty acid desaturase [Triticum aestivum]
16292	ENU00086	ANI61C5867: 1364..953	34-53	384-403	EST	"g6b11a1.r1, g6b11a1.fl"			34	0.39			(Z97208) putative Na/H exchanger [Schizosaccharomyces pombe]
16293	ENU00087	ANI61S716:4 41..25	28-47	378-402	EST	"e4b03a1.r1, e4b03a1.fl"			31	6			(AF061025) leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens]
16294	ENU00088	ANI61C4704: 435..1	55-74	428-447	EST	"x8e05a1.r1, x8e05a1.fl"			179	8E-45			"fructose-1,6-bisphosphatase (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) ; fructose-bisphosphatase (EC 3.1.3.11) - yeast (Saccharomyces cerevisiae) ; (Y00754) fructose-1,6-bisphosphatase (AA 1-348) [Saccharomyces cerevisiae] ; (J03207) fructose-1,6-bisphosphatase [Saccharomyces cerevisiae] ; (U19103) Fbp1p: fructose-1,6-bisphosphatase [Saccharomyces cerevisiae] "
16295	ENU00089	ANI61C8447: 1183..737	45-66	414-449	EST	"j9d02a1.r1, j9d02a1.fl"			32	2.2			(Z81095) predicted using Genefinder; cDNA EST EMBL:D71338 comes from this gene; cDNA EST EMBL:D74010 comes from this gene; cDNA EST EMBL:D74852 comes from this gene; cDNA EST EMBL:C07354 comes from this gene; cDNA EST EMBL:C086...

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvng	Description
16296	ENU00090	ANI61C2075: 23-42 137..584	23-42	404-428	EST	"g3b07a1.r1, g3b07a1.fl"			101	3E-21			24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
16297	ENU00091	ANI61C2075: 23-42 137..584	23-42	404-428	EST	"o9d11a1.r1, o9d11a1.fl"			101	3E-21			24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
16298	ENU00092	ANI61C7813: 50-69 1049..1498	50-69	438-457	EST	"y4h05a1.r1, y4h05a1.fl"			36	0.12			shed acute-phase antigen - Trypanosoma cruzi ; (X57235) shed-acute-phase-antigen [Trypanosoma cruzi]
16299	ENU00093	ANI61C1368: 22-53 613..1068	22-53	411-435	EST	"e0g12a1.r1, e0g12a1.fl"			31	5.2			hypothetical protein o259a - Escherichia coli ; (U14003) ORF_o259a [Escherichia coli] ; (AE000492) FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli]
16300	ENU00094	ANI61C1032 71-91 2:2226..1766	71-91	470-489	EST	"w8d12a1.r1, w8d12a1.fl"			73	1E-26			ADP-ribosylation factor ; ADP-ribosylation factor - Ajellomyces capsulata ; (L25117) ADP-ribosylation factor [Histoplasma capsulatum] (M19828) apolipoprotein B-100 precursor [Homo sapiens]
16301	ENU00095	ANI50C1088 27-49 6_1:855..391	27-49	417-449	EST	"x7d04a1.r1, x7d04a1.fl"			32	2.4			transcription factor MBP1 (MBF subunit P120) ; transcription factor MBP1 - yeast (Saccharomyces cerevisiae) ; (X74158) mbp1
16302	ENU00096	ANI61C6652: 39-58 1047..571	39-58	454-473	EST	"a0h02a1.r1, a0h02a1.fl"			33	1.4			transcription factor [Saccharomyces cerevisiae] ; (Z74104) ORF YDL056w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16303	ENU00097	ANI61C1710: 229..706	58-77	471-493	EST	"g5d09a1.r1, g5d09a1.fl"			32	1.9			(Z93377) cDNA EST EMBL:D65765 comes from this gene; cDNA EST EMBL:D69319 comes from this gene; cDNA EST yk235a4.3 comes from this gene; cDNA EST yk235a4.5 comes from this gene; cDNA EST yk414g2.5 comes from this gene [Caenorhab... ; (Z81513) cDNA EST EMBL:D65765 comes from this gene; cDNA EST EMBL:D69319 comes from this gene; cDNA EST yk235a4.3 comes from this gene; cDNA EST yk414g2.5 comes from this gene [Caenorhab... comes from this gene [Caenorhab... O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (AF017151) oxidoreductase [Aspergillus parasiticus] v-ski avian sarcoma viral oncogene homolog ; SKI oncogene (C-SKI) ; transforming protein ski - human ; (X15218) ski protein (AA 1 - 728) [Homo sapiens] "(AL031532) yeast grt2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe] "
16304	ENU00098	ANI61C6116: 129..612	44-69	456-485	EST	"y8f01a1.r1, y8f01a1.fl"			125	2E-28			
16305	ENU00099	ANI61C2195: 32-51 502..1	32-51	459-489	EST	"c7c05a1.r1, c7c05a1.fl"			32	2			
16306	ENU00100	ANI50C2350 0_1:322..845	23-45	480-504	EST	"i3a07a1.r1, i3a07a1.fl"			187	6E-47			
16307	ENU00101	ANI61C8673: 22-51 1620..2154	22-51	495-514	EST	"j0b04a1.r1, j0b04a1.fl"			32	3.8			
16308	ENU00102	ANI61C9863: 33-52 2554..2771	33-52	491-526	EST	"w8g10a1.r1, w8g10a1.fl"			40	0.01			[Escherichia coli] " Versican core protein precursor (large fibroblast proteoglycan) (chondroitin sulfate proteoglycan core protein 2) (PG-M) ; chondroitin sulfate proteoglycan PG-M core protein - chicken ; (D13542) proteoglycan [Gallus gallus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16309	ENU00103	ANI61C9440: 614..71	22-52	492-523	EST	"r1b12a1.r1, r1b12a1.fl"			114	2E-32			proteasome component PRE3 precursor (macropain subunit PRE3) (proteinase YSCE subunit PRE3) (multicatalytic endopeptidase complex subunit PRE3) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRE3 - yeast (Saccharomyces cerevisiae) ; (Z49276) ORF YJL001w [Saccharomyces cerevisiae]
16310	ENU00104	ANI61C1077 4:4466..3910	33-58	524-545	EST	"g3g03a1.r1, g3g03a1.fl"			50	0.00001			(U88181) similar to bovine PKR inhibitor P58 (GB:U04631); contains similarity to DNAL-like domain [Caenorhabditis elegans]
16311	ENU00105	ANI61C1044 5:38..594	55-74	549-569	EST	"r8f06a1.r1, r8f06a1.fl"			32	4			3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type IV (3beta-HSD IV) (3-beta-hydroxy-delta(5)-steroid dehydrogenase (3-beta-hydroxy-5-ene steroid dehydrogenase) (progesterone reductase) / steroid delta-isomeras... ; 3beta-hydroxysteroid-Delta5-steroid dehydrogenase multifunctional protein IV - rat ; (L17138) 3 hydroxysteroid dehydrogenase [Rattus norvegicus] (Z81579) Similarity to Schistosoma eggshell protein (SW:EGGS_SCHMA); cDNA EST EMBL:T01280 comes from this gene; cDNA EST EMBL:D69189 comes from this gene [Caenorhabditis elegans]
16312	ENU00106	ANI61C5291: 2703..2141	35-59	520-555	EST	"g3c03a1.r1, g3c03a1.fl"			33	1.4			"Glucosylase 1 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan GLUCOHydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) GAM1 - yeast (Schwanniomyces occidentalis) ; (M60207) glucosylase [Schwanniomyces occidentalis] " (D86051) carbonic anhydrase [Porphyridium purpureum]
16313	ENU00107	ANI61C4823: 3940..3364	28-55	529-561	EST	"i0g04a1.r1, i0g04a1.fl"			66	3E-10			
16314	ENU00108	ANI61C6961: 1292..1868	48-68	561-582	EST	"y8d10a1.r1, y8d10a1.fl"			129	1E-37			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16315	ENU00109	ANI61C2075: 22-46 1..584		539-563	EST	"v7h01a1.r1, v7h01a1.fl"			157	6E-38			24 KD metalloproteinase precursor (deuterolysin); metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus; (L37524) metalloproteinase [Aspergillus flavus] probable membrane protein YOL084w - yeast (Saccharomyces cerevisiae); (X83121) orf 00953 [Saccharomyces cerevisiae]; (Z74826) ORF YOL084w [Saccharomyces cerevisiae] (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana] glutathione peroxidase homolog YBR244W; probable glutathione peroxidase (EC 1.11.1.9) - yeast (Saccharomyces cerevisiae); (Z36113) ORF YBR244w [Saccharomyces cerevisiae] hypothetical protein YDR313c - yeast (Saccharomyces cerevisiae); (U28374) YDR313C gene product [Saccharomyces cerevisiae] (AB000276) DAP-1 beta [Homo sapiens] (D31844) cut9+ [Schizosaccharomyces pombe] "alpha-actinin, skeletal muscle isoform (F-actin cross linking protein); alpha-actinin 2, skeletal muscle splice form SK - chicken; (X59247) alpha-actinin [Gallus gallus]; (X13874) pectoralis alpha actinin [Gallus gallus]" (Y17393) prefoldin subunit 2 [Mus musculus] (AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum] 60S ribosomal protein L15; (Y15321) putative ribosomal protein L15 [Aspergillus niger]
16316	ENU00110	ANI61C5881: 34-54 3049..2462		557-579	EST	"g4a11a1.r1, g4a11a1.fl"			43	0.002			
16317	ENU00111	ANI61C5908: 46-69 1519..2119		575-604	EST	"t2d10a1.r1, t2d10a1.fl"			107	8E-23			
16318	ENU00112	ANI61C3455: 61-84 1338..1952		603-633	EST	"c7g02a1.r1, c7g02a1.fl"			191	4E-48			
16319	ENU00113	ANI61C1031 61-80 7:721..106		602-633	EST	"j9f07a1.r1, j9f07a1.fl"			59	0.000000 02			
16320	ENU00114	ANI61C1037 53-71 9:4710..4080		614-641	EST	"d5c05a1.r1, d5c05a1.fl"			36	0.19			
16321	ENU00115	ANI61C3140: 28-53 785..156		589-618	EST	"g3g05a1.r1, g3g05a1.fl"			31	6.3			
16322	ENU00116	ANI61C1046 50-75 4:3335..2700		616-643	EST	"j9f08a1.r1, j9f08a1.fl"			36	0.0001			
16323	ENU00117	ANI61C7547: 34-56 1827..2465		601-630	EST	"c8d04a1.r1, c8d04a1.fl"			63	0.000000 002			
16324	ENU00118	ANI61C7842: 32-51 820..174		618-636	EST	"o8e07a1.r1, o8e07a1.fl"			87	1E-16			
16325	ENU00119	ANI61C1119 22-50 4:1467..807		621-640	EST	"b0a07a1.r1, b0a07a1.fl"			155	2E-49			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16326	ENU00120	ANI61C4903: 1797..2461	24-46	619-646	EST	"l3a11a1.rl", l3a11a1.fl"			65	4E-20			"phosphoribosylglycinamide formyltransferase (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase) ; ADE8 protein - yeast (Saccharomyces cerevisiae) ; (M36585) ADE8 gene product [Saccharomyces cerevisiae] ; (U32274) Ade8p: glycineamide ribotide transformylase, EC number 2.1.2.2; YDR408C; CAI: 0.12 [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] "
16328	ENU00122	ANI61C9641: 22-42	22-42	634-661	EST	"r7f10a1.rl", r7f10a1.fl"			33	2.3			[Saccharomyces cerevisiae] "
16329	ENU00123	ANI61C6008: 22-46	22-46	639-673	EST	"z1f02a1.rl", z1f02a1.fl"			103	1E-40			(U78968) surface lipoprotein DppA [Streptococcus pyogenes] "ATP synthase subunit 4, mitochondrial precursor ; (AF019222) F1Fo-ATP synthase subunit 4 [Kluyveromyces lactis] "
16330	ENU00124	ANI61C1136: 29-48	29-48	662-684	EST	"fle10a1.rl", fle10a1.fl"			37	0.12			suppressor of hairy wing protein ; suppressor of hairy wing - fruit fly (Drosophila virilis) ; (Z25520) Hairy-wing protein [Drosophila virilis]
16331	ENU00125	ANI61C3096: 47-68	47-68	700-735	EST	"i8b09a1.rl", i8b09a1.fl"			268	2E-71			Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052) multifunctional beta-oxidation protein [Neurospora crassa]
16332	ENU00126	ANI61C580:2 87..1022	22-50	691-715	EST	"m0c07a1.rl", m0c07a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16333	ENU00127	ANI61C3096: 2180..1444	47-68	708-743	EST	"c8d05a1.r1, c8d05a1.fl"			268	2E-71			Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase; D-3-hydroxyacyl CoA dehydrogenase]; multifunctional beta-oxidation protein - Neurospora crassa; (X80052) multifunctional beta-oxidation protein [Neurospora crassa] (U91983) phosphatidylserine synthase [Triticum aestivum] putative signal recognition particle receptor beta subunit (SR-beta); probable purine nucleotide-binding protein YKL154w - yeast (Saccharomyces cerevisiae); (Z28154) ORF YKL154w [Saccharomyces cerevisiae]
16334	ENU00128	ANI61C5234: 1..759	22-54	719-738	EST	"g9f05a1.r1, g9f05a1.fl"			118	2E-53			
16335	ENU00129	ANI61C4904: 1320..556	22-52	720-744	EST	"r1f06a1.r1, r1f06a1.fl"			59	0.000000	03		
16336	ENU00130	ANI61C7349: 2376..1588	25-56	751-771	EST	"o0d07a1.r1, o0d07a1.fl"			34	1.7			Segment polarity protein dishevelled homolog DVL-1 (dishevelled-1) (DSH homolog 1); (U46461) cytoplasmic phosphoprotein [Homo sapiens] (AL022304) 40s ribosomal protein s16. [Schizosaccharomyces pombe] (AL022304) 40s ribosomal protein s16. [Schizosaccharomyces pombe] hypothetical protein H19-3' - mouse; (X58196) 3' ORF [Mus musculus] (Z49908) cDNA EST yk198d12.5 comes from this gene [Caenorhabditis elegans]
16337	ENU00131	ANI61C8418: 59..872	72-91	808-842	EST	"z4f02a1.r1, z4f02a1.fl"			106	9E-31			
16338	ENU00132	ANI61C6065: 831..3	72-91	835-858	EST	"d5g06a1.r1, d5g06a1.fl"			106	9E-31			
16339	ENU00133	ANI61C6065: 835..3	72-92	839-862	EST	"m2f09a1.r1, m2f09a1.fl"			32	4			
16340	ENU00134	ANI61C4936: 866..20	23-44	807-826	EST	"c9c04a1.r1, c9c04a1.fl"			32	4.2			
16341	ENU00135	ANI61C7423: 3162..4046	68-87	891-910	EST	"r1g10a1.r1, r1g10a1.fl"			37	0.22			adenylate cyclase (ATP pyrophosphate-lyase) (adenylyl cyclase); adenylate cyclase (EC 4.6.1.1) - Podospora anserina; (L43413) adenylyl cyclase [Podospora anserina]
16342	ENU00136	ANI61C7349: 1398..2303	22-55	862-885	EST	"i0a02a1.r1, i0a02a1.fl"							
16343	ENU00137	ANI61C6519: 674..1581	22-41	862-887	EST	"s9a11a1.r1, s9a11a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16344	ENU00138	ANI61C6671: 3857..2945	60-79	896-930	EST	"z5e07a1.r1, z5e07a1.fl"		39	0.045				(Z66499) T01B7.8 [Caenorhabditis elegans] (U94333) C1qR(p) [Homo sapiens]
16345	ENU00139	ANI61C2152: 1783..856	22-48	878-906	EST	"y8b10a1.r1, y8b10a1.fl"		34	2				
16346	ENU00140	ANI61C1035 9:1825..2753	22-52	888-908	EST	"d1a10a1.r1, d1a10a1.fl"		33	2.7				tRNA nucleotidyltransferase precursor (tRNA adenylyltransferase) (tRNA CCA-pyrophosphorylase) (CCA-adding enzyme); tRNA nucleotidyltransferase - yeast (Saccharomyces cerevisiae); (M59870) transfer RNA nucleotidyltransferase [Saccharomyces cerevisiae]; (U18922) Cca1p: tRNA nucleotidyltransferase(tRNA CCA-pyrophosphorylase) [Saccharomyces cerevisiae]
16347	ENU00141	ANI61C1049 7:4698..5643	43-72	927-946	EST	"y3a09a1.r1, y3a09a1.fl"							
16348	ENU00142	ANI61C2394: 2671..1698	68-88	965-999	EST	"o6d04a1.r1, o6d04a1.fl"		229	2E-79				(U76621) short-chain alcohol dehydrogenase [Aspergillus parasiticus]
16349	ENU00143	ANI61C4760: 993..18	43-65	957-976	EST	"d4a04a1.r1, d4a04a1.fl"		199	8E-71				"(AL034352) yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth and cytoskeletal or ganisation [Schizosaccharomyces pombe] "
16350	ENU00144	ANI61C1038 0:3175..4169	22-54	950-973	EST	"z3d02a1.r1, z3d02a1.fl"		61	0.000000	02			hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae); (Z71633) ORF YNR018w [Saccharomyces cerevisiae]
16351	ENU00145	ANI61C1038 0:3175..4169	22-54	950-973	EST	"i0h07a1.r1, i0h07a1.fl"		61	0.000000	02			hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae); (Z71633) ORF YNR018w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16352	ENU00146	ANI61C1038 0:3175..4169	22-54	950-973	EST	"x8b03a1.r1, x8b03a1.fl"		61	0.000000	02			hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae]
16353	ENU00147	ANI61C7944: 26-46 1993..993	26-46	965-987	EST	"r5a07a1.r1, r5a07a1.fl"		52	0.000005				hypothetical 37.8 KD protein in CLB6-SPT6 intergenic region ; hypothetical protein YGR113w - yeast (Saccharomyces cerevisiae) ; (Z72898) ORF YGR113w [Saccharomyces cerevisiae]
16354	ENU00148	ANI61C5297: 22-46 26..1067	22-46	1001-1020	EST	"g7g08a1.r1, g7g08a1.fl"		61	0.000000	02			(AL033497) unknown hypothetical protein [Candida albicans]
16355	ENU00149	ANI61C5363: 22-49 99..1143	22-49	996-1024	EST	"d3a01a1.r1, d3a01a1.fl"		109	2E-24				hypothetical 43.8 KD protein in NCE3-HHT2 intergenic region ; hypothetical protein YNL035c - yeast (Saccharomyces cerevisiae) ; (Z71311) ORF YNL035c [Saccharomyces cerevisiae]
16356	ENU00150	ANI61C1754: 22-51 4786..3743	22-51	1002-1024	EST	"y8e03a1.r1, y8e03a1.fl"		96	9E-26				(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
16357	ENU00151	ANI61C8138: 61-82 4412..3341	61-82	1060-1090	EST	"r5g03a1.r1, r5g03a1.fl"		371	e-102				"mitochondrial heat shock protein SSC1 precursor (endonuclease SCEI 75 KD subunit) ; heat shock protein 70-related protein SSC1 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (M27229) heat shock protein [Saccharomyces cerevisiae] ; (Z49545) ORF YJR045c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae] "
16358	ENU00152	ANI61C2761: 22-57 1220..113	22-57	1069-1088	EST	"x5a07a1.r1, x5a07a1.fl"		102	7E-42				(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
16359	ENU00153	ANI61C9617: 33-60 449..1617	33-60	1139-1159	EST	"o6e11a1.r1, o6e11a1.fl"		97	2E-19				(AL023776) hypothetical protein [Schizosaccharomyces pombe]
16360	ENU00154	ANI61C687:1 35-54 329..9	35-54	1294-1313	EST	"g6a09a1.r1, g6a09a1.fl"		45	0.001				(AF007190) intestinal mucin [Homo sapiens]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16361	ENU00155	ANI61C4155: 111..1470	22-42	1304-1339	EST	"c5b09a1.r1, c5b09a1.fl"			64	0.000000			ACTIN-like protein ARP9; probable membrane protein YMR033w - yeast (Saccharomyces cerevisiae); (Z49213) unknown [Saccharomyces cerevisiae] hypothetical 52.9 KD protein in SAP155-YMR31 intergenic region; hypothetical protein YFR044c - yeast (Saccharomyces cerevisiae); (D50617) YFR044C [Saccharomyces cerevisiae]; (D44597) unknown [Saccharomyces cerevisiae] eukaryotic translation initiation factor 2 alpha subunit (EIF-2-alpha); (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]
16362	ENU00156	ANI61C6712: 33-52 5596..4221	33-52	1341-1367	EST	"v7c12a1.r1, v7c12a1.fl"			405	e-133			
16363	ENU00157	ANI61C1040 9:3271..1880	34-61	1363-1382	EST	"z3b08a1.r1, z3b08a1.fl"			206	5E-58			(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe] probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin); (AL023859) putative ubiquitin protein ligase [Schizosaccharomyces pombe] extensin - almond; (X65718) extensin [Prunus dulcis]; extensin [Prunus dulcis] hypothetical 79.3 KD protein C24C9.05C in chromosome 1; (Z98601) hypothetical protein. [Schizosaccharomyces pombe] DNA repair protein RAD9; rad9 protein - fission yeast (Schizosaccharomyces pombe); rad9 protein - fission yeast (Schizosaccharomyces pombe); (X58231) rad9 protein [Schizosaccharomyces pombe]; (X64648) rad9 [Schizosaccharomyces pombe]; (X77276) rad9 [Schizosaccharomyces pombe]
16364	ENU00158	ANI61C1082 7:117..1551	54-73	1416-1446	EST	"h4a08a1.r1, h4a08a1.fl"			102	2E-22			
16365	ENU00159	ANI61C2461: 41-61 4436..2757	41-61	1653-1678	EST	"i3c07a1.r1, i3c07a1.fl"			199	6E-50			
16366	ENU00160	ANI61C9821: 22-48 4465..6193	22-48	1685-1708	EST	"j7b03a1.r1, j7b03a1.fl"			37	0.47			
16367	ENU00161	ANI61C844:2 176..380	22-45	1753-1776	EST	"i3h07a1.r1, i3h07a1.fl"			101	2E-39			
16368	ENU00162	ANI61C1001 4:243..2336	66-87	2084-2116	EST	"c4f11a1.r1, c4f11a1.fl"			64	6E-16			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16369	ENU00163	ANI61C8606: 137..2328	33-52	2151-2182	EST	"i2c03a1.r1, i2c03a1.fl"		48	0.0003				(AL034382) hypothetical serine rich protein [Schizosaccharomyces pombe]
16370	ENU00164	ANI61C1204: 45-65 1049..1248	45-65	181-202	EST	"y6g10a1.r1, y6g10a1.fl"		29	4.4				Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; (Z92539) eno [Mycobacterium tuberculosis] (D87063) chitinase [Emericella nidulans]
16371	ENU00165	ANI61C1083 32-51 4:2453..2254	32-51	164-189	EST	"m7h01a1.r1, m7h01a1.fl"		31	1.1				Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; (Z92539) eno [Mycobacterium tuberculosis]
16372	ENU00166	ANI61C1204: 39-59 1049..1248	39-59	175-196	EST	"m5e12a1.r1, m5e12a1.fl"		29	4.4				Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; (Z92539) eno [Mycobacterium tuberculosis]
16373	ENU00167	ANI61C1204: 44-64 1049..1248	44-64	180-201	EST	"o0g12a1.r1, o0g12a1.fl"		29	4.4				Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; (Z92539) eno [Mycobacterium tuberculosis]
16374	ENU00168	ANI61C1035 22-40 4:2463..2564	22-40	155-180	EST	"x8g04a1.r1, x8g04a1.fl"		29	3.3				serine/threonine-protein kinase SNK (serum inducible kinase) ; serum-inducible kinase - mouse (U39501) OrfB; IS3 family OrfB proteins homolog; Method: conceptual translation supplied by author. [Caulobacter crescentus]
16375	ENU00169	ANI61C4983: 27-45 129..338	27-45	170-194	EST	"y8e10a1.r1, y8e10a1.fl"		31	1.1				"Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emericella nidulans] ; dehydrogenase,aldehyde [Emericella nidulans] "
16376	ENU00170	ANI61C4777: 41-60 1063..849	41-60	193-213	EST	"o8c07a1.r1, o8c07a1.fl"		120	1E-27				"Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emericella nidulans] ; dehydrogenase,aldehyde [Emericella nidulans] "
16377	ENU00171	ANI61C4777: 41-60 1063..849	41-60	193-213	EST	"r5b09a1.r1, r5b09a1.fl"		120	1E-27				"Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emericella nidulans] ; dehydrogenase,aldehyde [Emericella nidulans] "
16378	ENU00172	ANI61C1083 60-79 4:2503..2279	60-79	218-242	EST	"a0f05a1.r1, a0f05a1.fl"		66	3E-11				(D87063) chitinase [Emericella nidulans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16379	ENU00173	ANI61C3868: 50-69 1613..1836	50-69	212-232	EST	"g2b07a1.r1, g2b07a1.fl"			31	1.7			(AF130745) regulator of G-protein signalling LOCO C1 [Drosophila melanogaster]
16380	ENU00174	ANI61C8080: 56-75 949..1178	56-75	219-243	EST	"x7g02a1.r1, x7g02a1.fl"			31	1.9			asparagine/glutamine permease ; probable membrane protein YCL025c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL025c: len:633 [Saccharomyces cerevisiae]
16381	ENU00175	ANI61C2092: 58-77 491..258	58-77	229-249	EST	"h4c02a1.r1, h4c02a1.fl"			31	1.1			hypothetical 41.6 KD protein in CSIE-GLYA intergenic region ; (AE000340) MFS (major facilitator superfamily) transporter [Escherichia coli] ; (D90883) similar to [SwissProt Accession Number P44629] [Escherichia coli] ; (D90884) similar to [SwissProt Accession Number P44629] [Escherichia coli]
16382	ENU00176	ANI61C3827: 52-71 560..317	52-71	233-253	EST	"l0d10a1.r1, l0d10a1.fl"			49	0.000005			Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae]
16383	ENU00177	ANI61C2572: 45-65 331..574	45-65	227-246	EST	"l0c11a1.r1, l0c11a1.fl"			31	1.3			putative 3-methyladenine DNA glycoylase ; (Z95117) hypothetical protein MLC1351.17c [Mycobacterium leprae]
16384	ENU00178	ANI61C8119: 39-58 779..536	39-58	219-240	EST	"p0g10a1.r1, p0g10a1.fl"			31	1.6			(Z74033) F38B7.4 [Caenorhabditis elegans]
16385	ENU00179	ANI61C7674: 54-87 5430..5186	54-87	232-256	EST	"l3a10a1.r1, l3a10a1.fl"			29	5			Chitin synthase 1 (chitin-UDP acetyl-glucosaminyl transferase 1) ; chitin synthase (EC 2.4.1.16) - yeast (Saccharomyces cerevisiae) ; (M14045) chitin synthase [Saccharomyces cerevisiae] ; (Z71468) ORF YNL192w [Saccharomyces cerevisiae]
16386	ENU00180	ANI61C3796: 22-50 1875..1628	22-50	208-227	EST	"z4b03a1.r1, z4b03a1.fl"			32	0.59			hypothetical 8.9 KD protein in INT-C1 intergenic region (ORF3) (ORF17) ; hypothetical protein 17 - phage HP1 ; hypothetical protein 3 - phage HP1 ; (U24159) orf3 [Bacteriophage HP1] Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum] "
16387	ENU00181	ANI61C3827: 52-71 560..310	52-71	240-260	EST	"j9c08a1.r1, j9c08a1.fl"			49	0.000006			
16388	ENU00182	ANI61C3054: 63-82 2259..2511	63-82	244-273	EST	"m2e09a1.r1, m2e09a1.fl"			40	0.004			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16389	ENU00183	ANI61C8048: 627..882	41-61	220-254	EST	"z1e09a1.r1, z1e09a1.fl"			29	7.2			(AF025847) (p)ppGpp synthetase [Myxococcus xanthus]
16390	ENU00184	ANI50C3665 52-71	52-71	256-275	EST	"m8d06a1.r1, m8d06a1.fl"			32	1.2			(U39501) OrfB; IS3 family OrfB proteins homolog; Method: conceptual translation supplied by author. [Caulobacter crescentus]
16391	ENU00185	ANI61C4983: 0_1:497..232 42..311	63-82	266-290	EST	"r5c08a1.r1, r5c08a1.fl"			31	3.1			Alkanal monooxygenase alpha chain (bacterial luciferase alpha chain) ; alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - flashlight fish symbiont bacterium ; (M36597) luciferase-alpha subunit [Kryptophanaron alfredi symbiont] (U86920) similar to variola A13L and vaccinia A12L [Molluscum contagiosum virus subtype 1]
16393	ENU00187	ANI61C175:3 56..653	23-42	239-267	EST	"c5b11a1.r1, c5b11a1.fl"			29	9.2			(AF052248) fork head domain protein FKD5 [Danio rerio]
16394	ENU00188	ANI61C9221: 1598..1887	68-88	283-315	EST	"t2e10a1.r1, t2e10a1.fl"			33	0.66			metallothionein-like protein 1 ; metallothionein - barley ; (X58540) ids-1 [Hordeum vulgare]
16395	ENU00189	ANI61C1688: 73..369	27-46	259-281	EST	"y6c12a1.r1, y6c12a1.fl"			36	0.1			metallothionein-like protein 1 ; metallothionein - barley ; (X58540) ids-1 [Hordeum vulgare]
16396	ENU00190	ANI61C5649: 160..461	25-44	265-284	EST	"c8f03a1.r1, c8f03a1.fl"			36	0.1			metallothionein-like protein 1 ; metallothionein - barley ; (X58540) ids-1 [Hordeum vulgare]
16397	ENU00191	ANI61C5649: 160..461	25-44	265-284	EST	"c5b02a1.r1, c5b02a1.fl"			36	0.11			metallothionein-like protein 1 ; metallothionein - barley ; (X58540) ids-1 [Hordeum vulgare]
16398	ENU00192	ANI61C5649: 154..461	25-44	271-290	EST	"z1c03a1.r1, z1c03a1.fl"			36	0.11			(AF003140) weak similarity to the drosophila hyperplastic disc protein (GB:L14644) [Caenorhabditis elegans]
16399	ENU00193	ANI61C7214: 614..923	72-89	320-339	EST	"w6d12a1.r1, w6d12a1.fl"			33	0.87			
16400	ENU00194	ANI61C1065 9:1234..1569	34-53	304-327	EST	"x9h11a1.r1, x9h11a1.fl"							
16401	ENU00195	ANI61C6234: 825..479	43-62	324-347	EST	"r5c03a1.r1, r5c03a1.fl"							
16402	ENU00196	ANI61C8131: 642..292	23-42	312-331	EST	"g5a04a1.r1, g5a04a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16403	ENU00197	ANI61C992:1 562..1920	69-87	366-385	EST	"g6g12a1.rl, g6g12a1.fl"							
16404	ENU00198	ANI61C9858: 58-77 169..538	58-77	366-385	EST	"k0b04a1.rl, k0b04a1.fl"		34	0.43				(AE000831) conserved protein [Methanobacterium thermoautotrophicum]
16405	ENU00199	ANI61C2656: 59-78 1399..1494	59-78	369-388	EST	"j7h07a1.rl, j7h07a1.fl"							
16406	ENU00200	ANI61C8448: 22-43 488..116	22-43	332-352	EST	"w8g03a1.rl, w8g03a1.fl"							
16407	ENU00201	ANI61C9663: 66-85 2362..1988	66-85	368-398	EST	"r2d02a1.rl, r2d02a1.fl"		34	0.44				cold-regulated protein cor15b precursor - Arabidopsis thaliana ; (AC007087)
16408	ENU00202	ANI61C2177: 71-90 429..51	71-90	388-407	EST	"n0g07a1.rl, n0g07a1.fl"		35	0.26				cold-regulated protein cor15b precursor [Arabidopsis thaliana]
16409	ENU00203	ANI61C6321: 55-74 729..1115	55-74	377-399	EST	"q0h02a1.rl, q0h02a1.fl"		31	4.1				N-methyl-D-aspartate receptor subunit NR2C - mouse ; (L35029) N-methyl-D-aspartate receptor subunit NR2C [Mus musculus]
16410	ENU00204	ANI61C7538: 55-74 1408..1019	55-74	381-402	EST	"d1a12a1.rl, d1a12a1.fl"		55	0.000000	2			(D14289) MTG8 protein [Homo sapiens]
16411	ENU00205	ANI61C346:2 40-59 429..2826	40-59	373-394	EST	"p0g07a1.rl, p0g07a1.fl"		32	1.4				(AF021797) peroxisomal receptor for PTS2-containing proteins Pex7p [Pichia pastoris]
16412	ENU00206	ANI61C1677: 23-43 8849..8450	23-43	357-380	EST	"o6a03a1.rl, o6a03a1.fl"		31	3.3				(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]
16413	ENU00207	ANI61C1064 59-78 9:793..391	59-78	399-419	EST	"r6c07a1.rl, r6c07a1.fl"		94	6E-19				(U70038) ICP0B [Human herpesvirus 1]
16414	ENU00208	ANI61C8117: 41-60 520..924	41-60	383-403	EST	"w7f07a1.rl, w7f07a1.fl"							(D89340) dipeptidyl peptidase III [Rattus norvegicus]
16415	ENU00209	ANI61C2656: 26-45 1033..1440	26-45	372-391	EST	"o4b07a1.rl, o4b07a1.fl"		32	2				(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16416	ENU00210	ANI61C3182: 58-79 4557..4965			EST	"j4b05a1.r1, j4b05a1.fl"			157	5E-38			cystathionine gamma-lyase (gamma-cystathionase); cystathionine gamma-lyase (EC 4.4.1.1) - yeast (Saccharomyces cerevisiae) ; (L05146) Cys3p: cystathionine gamma-lyase [Saccharomyces cerevisiae] ; (D14135) cystathionine gamma-lyase [Saccharomyces cerevisiae] ; (L04459) cystathionine gamma-lyase [Saccharomyces cerevisiae] (U40790) vascular protein tyrosine phosphatase 1 [Rattus norvegicus] (AL049498) putative transcription factor [Schizosaccharomyces pombe] hypothetical 112.0 KD protein C1F3.03 in chromosome I ; (Z70690) unknown [Schizosaccharomyces pombe] (Z99120) yurE [Bacillus subtilis] (U56098) FacB [Aspergillus oryzae] (U80844) strong similarity to amino-terminal 80 aa of aldehyde reductases [Caenorhabditis elegans] Fimbrin-like protein FIMI ; fimbrial protein FimI - Salmonella typhi ; (X74064) FimI protein [Salmonella typhi] Periodic tryptophan protein 1 ; PWP1 protein - yeast (Saccharomyces cerevisiae) ; (M37578) periodic tryptophan protein [Saccharomyces cerevisiae] ; (U14913) Pwp1p [Saccharomyces cerevisiae] ; periodic Trp protein [Saccharomyces cerevisiae]
16417	ENU00211	ANI61C9024: 41-60 5175..5584		381-408	EST	"g9h09a1.r1, g9h09a1.fl"		31		3.4			
16418	ENU00212	ANI61C8749: 56-75 1001..591		399-424	EST	"c4f09a1.r1, c4f09a1.fl"		32		1.5			
16419	ENU00213	ANI61C9005: 68-87 1114..692		427-448	EST	"l3a12a1.r1, l3a12a1.fl"		41		0.004			
16420	ENU00214	ANI61C746:1 68-91 493..1065		434-454	EST	"e0d12a1.r1, e0d12a1.fl"		31		6.2			
16421	ENU00215	ANI61C9771: 23-42 3408..2966		389-423	EST	"o0e05a1.r1, o0e05a1.fl"		32		2.9			
16422	ENU00216	ANI61C3900: 71-92 332..777		456-475	EST	"b0b10a1.r1, b0b10a1.fl"		30		8.6			
16423	ENU00217	ANI61C9823: 26-46 7232..6813		411-435	EST	"w6c11a1.r1, w6c11a1.fl"		31		3.9			
16424	ENU00218	ANI61C1113 72-91 7:459..915		466-486	EST	"y8b01a1.r1, y8b01a1.fl"		63		0.000000 001			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16425	ENU00219	ANI61C8906: 436..893	68-87	455-483	EST	"c9d01a1.rl, c9d01a1.fl"			32	2.3			"(Z70204) predicted using GeneFinder; similar to Zinc finger, C4 type (two domains); cDNA EST EMBL:T00457 comes from this gene; cDNA EST EMBL:C09248 comes from this gene; cDNA EST EMBL:C07758 comes from this gene; cDNA EST yk261... " (U66220) unknown [Nannocystis excelsus] (AF044025) circumsporozoite protein [Apicomplexa sp. 72141] hypothetical 62.8 KD protein in SSE1-CAR1 intergenic region ; probable membrane protein YPL109c - yeast (Saccharomyces cerevisiae) ; (U43503) Lph17p [Saccharomyces cerevisiae] major cold shock protein CSPA ; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] major cold shock protein CSPA ; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] major cold shock protein CSPA ; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] major cold shock protein CSPA ; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] TEF5 protein - yeast (Saccharomyces cerevisiae)
16426	ENU00220	ANI61C1067 2:467..1	30-49	426-454	EST	"o0a09a1.rl, o0a09a1.fl"			34	0.62			
16427	ENU00221	ANI61C3179: 1628..2095	66-85	471-491	EST	"w9e07a1.rl, w9e07a1.fl"			31	5.4			
16428	ENU00222	ANI61C6422: 1787..2263	47-66	461-481	EST	"c3a02a1.rl, c3a02a1.fl"			90	6E-18			
16429	ENU00223	ANI61C4792: 766..289	23-42	439-458	EST	"v7c02a1.rl, v7c02a1.fl"			60	0.000000 009			
16430	ENU00224	ANI61C4792: 766..289	39-58	455-474	EST	"w9h11a1.rl, w9h11a1.fl"			60	0.000000 009			
16431	ENU00225	ANI61C4792: 766..289	23-42	439-458	EST	"m0b05a1.rl, m0b05a1.fl"			60	0.000000 009			
16432	ENU00226	ANI61C4792: 766..289	25-44	441-460	EST	"q0e01a1.rl, q0e01a1.fl"			60	0.000000 009			
16433	ENU00227	ANI61C8456: 3363..3842	49-68	461-486	EST	"c3h01a1.rl, c3h01a1.fl"			114	3E-25			
16434	ENU00228	ANI61C7916: 1409..930	48-67	461-485	EST	"y8e09a1.rl, y8e09a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16435	ENU00229	ANI61C6190: 231..716	37-55	460-480	EST	"h1h04a1.r1, h1h04a1.fl"		59	0.000000	03			Gcy protein ; Gcy1 protein - yeast (Saccharomyces cerevisiae) ; (X13228)
													Gcy protein (AA 1-312)
													[Saccharomyces cerevisiae] ; (X90518)
													ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w
													[Saccharomyces cerevisiae] ; (X96740)
													Gcy protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w
													[Saccharomyces cerevisiae]
16436	ENU00230	ANI61C6237: 62-81	62-81	494-512	EST	"t2e09a1.r1, t2e09a1.fl"		100	1E-23				(D78151) human 26S proteasome subunit p97 [Homo sapiens]
16437	ENU00231	ANI61C8962: 41..533	65-84	504-523	EST	"c3h03a1.r1, c3h03a1.fl"		257	3E-68				"AMP deaminase (myoadenylate deaminase) ; AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae) ; (Z46659) AMD1 gene, len: 810, CAl: 0.19, AMP deaminase [Saccharomyces cerevisiae]"
16438	ENU00232	ANI61C9646: 46-65	46-65	486-506	EST	"n8c05a1.r1, n8c05a1.fl"		85	4E-16				(Z99532) putative vacuolar h(+)-atpase subunit [Schizosaccharomyces pombe]
16439	ENU00233	ANI61C1040: 671..169	48-67	492-513	EST	"j0d02a1.r1, j0d02a1.fl"		82	1E-17				methionine aminopeptidase 2 (METAP 2) (peptidase M 2) ; (U17437)
		4:2382..1875											methionine aminopeptidase 2 [Saccharomyces cerevisiae]
16440	ENU00234	ANI61C1041: 9:1472..958	48-67	496-520	EST	"n0a05a1.r1, n0a05a1.fl"		31	8.2				[Saccharomyces cerevisiae]
													ribonucleoprotein - Arabidopsis thaliana ; (M98340) ribonucleoprotein [Arabidopsis thaliana] ; Ser/Arg-rich protein [Arabidopsis thaliana]
16441	ENU00235	ANI61C5819: 50-69	50-69	495-527	EST	"y8b12a1.r1, y8b12a1.fl"		31	4.8				(AF003696) cellulase A [Cellvibrio mixtus]
16442	ENU00236	ANI61C7241: 1019..1538	46-65	505-531	EST	"k0d10a1.r1, k0d10a1.fl"		35	0.43				probable membrane protein YPL162c - yeast (Saccharomyces cerevisiae) ; (Z73518) ORF YPL162c
		2240..1713											[Saccharomyces cerevisiae] ; (X96770) P2558 protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16443	ENU00237	ANI61C7054: 1373..835	55-74	532-551	EST	"z5f1a1.rl, z5f1a1.fl"			201	4E-51				"Dihydroxy-acid dehydratase precursor (DAD) (2,3-dihydroxy acid hydrolyase) ; dihydroxy-acid dehydratase (EC 4.2.1.9) - yeast (Saccharomyces cerevisiae) ; (X87611) dihydroxyacid dehydratase [Saccharomyces cerevisiae] ; (Z49516) ORF YJR016c [Saccharomyces cerevisiae]"
16444	ENU00238	ANI61C1560: 6167..5623	70-89	543-572	EST	"z3c05a1.rl, z3c05a1.fl"			32	3.9				(AF013294) contains similarity to gag proteins [Arabidopsis thaliana]
16445	ENU00239	ANI61C1560: 6167..5623	70-89	543-572	EST	"o8d01a1.rl, o8d01a1.fl"			32	3.9				(AF013294) contains similarity to gag proteins [Arabidopsis thaliana]
16446	ENU00240	ANI61C7674: 22-44	507-530	EST		"l3a10a1.rl, l3a10a1.fl"			31	8.9				(AF016833) maltase-glucoamylase [Homo sapiens]
16447	ENU00241	ANI61C8356: 3042..2482	35-54	527-553	EST	"o6f04a1.rl, o6f04a1.fl"			76	3E-28				"dismutase,Mn superoxide [Saccharomyces cerevisiae]"
16448	ENU00242	ANI61C8356: 3042..2478	35-54	535-557	EST	"g4h09a1.rl, g4h09a1.fl"			76	3E-28				"dismutase,Mn superoxide [Saccharomyces cerevisiae]"
16449	ENU00243	ANI61C1031 3:1608..1745	61-81	568-585	EST	"e4b04a1.rl, e4b04a1.fl"								
16450	ENU00244	ANI61C2396: 3584..3002	56-75	577-596	EST	"c9h09a1.rl, c9h09a1.fl"			31	9.6				major blood-stage surface antigen Pv200 - Plasmodium vivax ; (M75674)
16451	ENU00245	ANI61C7700: 782..191	63-80	579-612	EST	"j7c03a1.rl, j7c03a1.fl"			66	9E-20				Pv200 [Plasmodium vivax] Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
16452	ENU00246	ANI61C7916: 1521..930	34-53	559-583	EST	"p0c05a1.rl, p0c05a1.fl"			63	0.000000				(AF010288) synaptobrevin [Aspergillus parasiticus]
16453	ENU00247	ANI61C5247: 2462..1859	29-62	559-590	EST	"c5c06a1.rl, c5c06a1.fl"			37	0.13				"Myristoylated alanine-rich C-kinase substrate (MARCKS) (protein kinase C substrate, 80 KD protein, light chain) (PKCSL) (80K-L protein) ; myristoylated alanine-rich protein kinase C substrate - human ; (D10522) 80K-L protein [Homo sapiens]"
16454	ENU00248	ANI61C2967: 932..1542	61-80	608-629	EST	"l0c09a1.rl, l0c09a1.fl"			35	0.53				laminin chain A - fruit fly (Drosophila melanogaster) (fragment) ; (M75882) laminin A chain [Drosophila melanogaster]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16455	ENU00249	ANI61C3552: 812..198	53-72	597-625	EST	"c9b04a1.r1, c9b04a1.fl"		56	3E-15				(AF047694) glutaredoxin [Vernicia fordii]
16456	ENU00250	ANI61C6038: 1052..1684	23-50	594-613	EST	"r5b05a1.r1, r5b05a1.fl"		45	0.0004				probable membrane protein YLR326w - yeast (Saccharomyces cerevisiae) ; (U20618) Ylr326wp [Saccharomyces cerevisiae]
16457	ENU00251	ANI61C1626: 1081..444	33-52	605-625	EST	"j4b03a1.r1, j4b03a1.fl"		34	0.95				(AF055943) NADH dehydrogenase subunit II [Anolis limifrons]
16458	ENU00252	ANI61C6038: 1039..1684	22-47	606-625	EST	"g9d06a1.r1, g9d06a1.fl"		45	0.0004				probable membrane protein YLR326w - yeast (Saccharomyces cerevisiae) ; (U20618) Ylr326wp [Saccharomyces cerevisiae]
16459	ENU00253	ANI61C6038: 1039..1684	22-47	606-625	EST	"r7g05a1.r1, r7g05a1.fl"		45	0.0004				probable membrane protein YLR326w - yeast (Saccharomyces cerevisiae) ; (U20618) Ylr326wp [Saccharomyces cerevisiae]
16460	ENU00254	ANI61C4165: 1476..2131	72-92	659-685	EST	"g6d05a1.r1, g6d05a1.fl"		182	3E-45				(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermitis]
16461	ENU00255	ANI61C6835: 3100..2443	63-83	659-678	EST	"o6d01a1.r1, o6d01a1.fl"		34	0.76				(U58951) envelope polypeptide [Feline leukemia virus]
16462	ENU00256	ANI61C4073: 414..4078	31-50	633-653	EST	"w4b06a1.r1, w4b06a1.fl"		47	1E-14				(AE001038) enoyl-CoA hydratase (fad-3) [Archaeoglobus fulgidus]
16463	ENU00257	ANI61C7842: 110..774	22-41	625-644	EST	"g7c10a1.r1, g7c10a1.fl"		80	1E-14				(AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum]
16464	ENU00258	ANI61C2915: 949..1627	22-40	636-658	EST	"x7b08a1.r1, x7b08a1.fl"		78	6E-16				cytochrome C oxidase polypeptide VIB (AED) ; cytochrome-c oxidase (EC 1.9.3.1) chain Vlb - yeast (Saccharomyces cerevisiae) ; (M98332) cytochrome c oxidase subunit Vlb [Saccharomyces cerevisiae] ; (Z73210) ORF YLR038c [Saccharomyces cerevisiae]
16465	ENU00259	ANI61C1043: 6:3221..3901	44-63	654-682	EST	"x9f03a1.r1, x9f03a1.fl"		36	0.35				HKR1 protein precursor - yeast (Saccharomyces cerevisiae) ; (U33007) Hkr1p; YDR420W; CAI: 0.10 [Saccharomyces cerevisiae]
16466	ENU00260	ANI61C6415: 7150..7845	25-44	659-678	EST	"z4e10a1.r1, z4e10a1.fl"		36	0.00003				hypothetical protein 5 - Xanthobacter sp ; (X79863) orf5 [Xanthobacter sp. Py2]

Seq num	Seq id	Primer 5 pos	Contig Source	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16467	ENU00261	ANI61C2721: 72-91	ANI61C2721: 1465..738	735-756	EST	"w4a08a1.r1, w4a08a1.fl"		57	0.000000	1			(Z97185) hypothetical protein [Schizosaccharomyces pombe]
16468	ENU00262	ANI61C7657: 68-87	ANI61C7657: 748..1486	745-764	EST	"r7c05a1.r1, r7c05a1.fl"		34	1.2	1.2			(L26122) matrix protein [Mumps virus]
16469	ENU00263	ANI61C5855: 25-44	ANI61C5855: 3097..3837	704-723	EST	"i8g07a1.r1, i8g07a1.fl"		34	1.5	1.5			(L13855) UL3.5 [Pseudorabies virus]
16470	ENU00264	ANI61C9566: 24-44	ANI61C9566: 730..1501	722-753	EST	"c1c12a1.r1, c1c12a1.fl"							
16471	ENU00265	ANI61C1704: 68-87	ANI61C1704: 827..51	783-802	EST	"f0h12a1.r1, f0h12a1.fl"		122	2E-47	2E-47			"40S ribosomal protein S18E ; ribosomal protein S18.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z46659) 40S ribosomal protein gene, len: 146, CAl: 0.74 [Saccharomyces cerevisiae] ; (U33007) Ydr450wp [Saccharomyces cerevisiae] "
16472	ENU00266	ANI61C8446: 39-58	ANI61C8446: 1107..1885	750-775	EST	"i0g02a1.r1, i0g02a1.fl"		38	0.11	0.11			mucin (clone PGM-2A) - pig ; gastric mucin - pig (fragment) ; (U10281) gastric mucin [Sus scrofa]
16473	ENU00267	ANI61C3644: 32-51	ANI61C3644: 2753..3532	750-769	EST	"m0a12a1.r1, m0a12a1.fl"		126	2E-28	2E-28			hypothetical protein 1 - Pseudomonas cepacia ; (U19883) unknown [Burkholderia cepacia]
16474	ENU00268	ANI61C6750: 45-64	ANI61C6750: 2437..2657	783-802	EST	"z4h02a1.r1, z4h02a1.fl"		36	0.25	0.25			"Dynactin, 117 KD isoform ; dynactin - chicken ; (X62773) dynactin [Gallus sp.] "
16475	ENU00269	ANI61C3540: 27-62	ANI61C3540: 1573..772	767-786	EST	"r7h08a1.r1, r7h08a1.fl"		32	5	5			probable membrane protein YOR086c - yeast (Saccharomyces cerevisiae) ; (X94335) YOR3141c [Saccharomyces cerevisiae] ; (Z74994) ORF YOR086c [Saccharomyces cerevisiae]
16476	ENU00270	ANI61C1048	ANI61C1048	29-48	EST	"o6c11a1.r1, o6c11a1.fl"		65	5E-10	5E-10			"(D90835) H-NS-repressed protein, 30K [Escherichia coli] "
16477	ENU00271	ANI50C4955	ANI50C4955	815-836	EST	"i0a07a1.r1, i0a07a1.fl"		35	0.77	0.77			nucleocapsid protein - phocine distemper virus
16478	ENU00272	ANI61C4457: 23-42	ANI61C4457: 164..985	784-802	EST	"d5g03a1.r1, d5g03a1.fl"		85	2E-22	2E-22			(AL035528) putative protein [Arabidopsis thaliana]
16479	ENU00273	ANI61C8325: 26-46	ANI61C8325: 2353..1515	803-822	EST	"z3b12a1.r1, z3b12a1.fl"		32	6.9	6.9			(U90878) carboxyl terminal LIM domain protein [Homo sapiens]
16480	ENU00274	ANI61C6322: 49-68	ANI61C6322: 176..1022	834-853	EST	"g2a01a1.r1, g2a01a1.fl"		34	1.4	1.4			(AF024502) No definition line found [Caenorhabditis elegans]
16481	ENU00275	ANI61C7455: 22-41	ANI61C7455: 307..1160	814-833	EST	"g5g12a1.r1, g5g12a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16482	ENU00276	ANI61C878:2 051..1195	53-72	845-867	EST	"y6g06a1.r1, y6g06a1.fl"							
16483	ENU00277	ANI61C878:2 051..1195	44-63	836-858	EST	"y8e02a1.r1, y8e02a1.fl"							
16484	ENU00278	ANI61C878:2 051..1195	53-72	845-867	EST	"o8h12a1.r1, o8h12a1.fl"							
16485	ENU00279	ANI61C7147: 5139..6007	72-92	879-898	EST	"h4a04a1.r1, h4a04a1.fl"							
16486	ENU00280	ANI61C1473: 3691..4569	63-82	875-899	EST	"h1g02a1.r1, h1g02a1.fl"							
16487	ENU00281	ANI61C3452: 933..65	33-52	860-879	EST	"d5b06a1.r1, d5b06a1.fl"							
16488	ENU00282	ANI61C6527: 4147..3252	58-77	887-911	EST	"i2a02a1.r1, i2a02a1.fl"							
16489	ENU00283	ANI61C6529: 4358..5265	70-88	916-935	EST	"j9f03a1.r1, j9f03a1.fl"							
16490	ENU00284	ANI61C1023: 2980..2071	64-83	905-930	EST	"o6c05a1.r1, o6c05a1.fl"							
16491	ENU00285	ANI61C6339: 2287..1364	44-63	906-925	EST	"b0e10a1.r1, b0e10a1.fl"							
16492	ENU00286	ANI61C9112: 1258..2202	34-53	911-936	EST	"l3e12a1.r1, l3e12a1.fl"							
16493	ENU00287	ANI61C2746: 36..983	57-76	933-962	EST	"h4b10a1.r1, h4b10a1.fl"							
								64	0.000000	002			"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]"
								32	4.6				(Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Config Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16494	ENU00288	ANI61C7396: 30-49 5964..5008		923-944	EST	"m6h01a1.r1, m6h01a1.fl"		46	0.0005				cytochrome C oxidase polypeptide VIA precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VIa precursor - yeast (Saccharomyces cerevisiae) ; (X72970) cytochrome-c oxidase [Saccharomyces cerevisiae] ; (X91837) cytochrome-C oxidase chain VIa precursor [Saccharomyces cerevisiae] ; (Z72713) ORF YGL191w [Saccharomyces cerevisiae]
16495	ENU00289	ANI61C8213: 69-88 915..1006		966-985	EST	"g4a02a1.r1, g4a02a1.fl"		133	2E-30				(L06279) HOG1 protein [Saccharomyces cerevisiae]
16496	ENU00290	ANI61C352:9 45-63 115..10082		943-970	EST	"x5e08a1.r1, x5e08a1.fl"		79	4E-14				hypothetical protein YOL071w - yeast (Saccharomyces cerevisiae) ; (Z74813) ORF YOL071w [Saccharomyces cerevisiae]
16497	ENU00291	ANI61C1713: 33-51 224..1196		944-963	EST	"z1f05a1.r1, z1f05a1.fl"		112	4E-24				"ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae]"
16498	ENU00292	ANI61C1510: 54-73 2838..2784		985-1006	EST	"d5f06a1.r1, d5f06a1.fl"		36	0.56				(U52210) outer membrane protein; OmpH [Pasteurella multocida]
16499	ENU00293	ANI61C560:1 66-85 41..1141		1004-1023	EST	"j9h05a1.r1, j9h05a1.fl"		35	0.97				(AL031262) hypothetical protein [Schizosaccharomyces pombe]
16500	ENU00294	ANI61C6754: 43-62 4129..5153		1002-1025	EST	"i7f03a1.r1, i7f03a1.fl"		276	2E-73				probable oxidoreductase C26F1.07 in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe]
16501	ENU00295	ANI61C8915: 23-42 1890..846		1006-1025	EST	"y8a06a1.r1, y8a06a1.fl"		57	0.000000				X-Ray Structure Of Bacteriorhodopsin From Microcrystals Grown In Lipidic Cubic Phases
16502	ENU00296	ANI61C9104: 60-79 2033..3112		1061-1093	EST	"o6b05a1.r1, o6b05a1.fl"		68	3E-22				hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16503	ENU00297	ANI61C1724: 56-77 2733..3814		1074-1095	EST	"o6d03a1.r1, o6d03a1.fl"			233	2E-60			"vacuolar aminopeptidase I precursor (polypeptidase) (leucine aminopeptidase IV) (LAPIV) (aminopeptidase III) (aminopeptidase YSC1) ; aminopeptidase ysc1 (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae) ; (M25548) aminopeptidase I [Saccharomyces cerevisiae] ; (X71133) vacuolar aminopeptidase YSC1 [Saccharomyces cerevisiae] ; (Z28103) ORF YKL103c [Saccharomyces cerevisiae] "
16504	ENU00298	ANI61C8591: 56-75 4826..3741		1078-1098	EST	"w8e01a1.r1, w8e01a1.fl"		35	1.1				"(U50191) C. elegans collagen dpy-10 gene (Levy, A.D., Yang, J. and Kramer, J.M. Mol. Biol. Cell 4, 803-17, 1993) [Caenorhabditis elegans] "
16505	ENU00299	ANI61C1649: 57-76 1879..782		1090-1112	EST	"g5e01a1.r1, g5e01a1.fl"		198	8E-50				"serine/threonine-protein kinase SAT4 ; probable protein kinase YCR008w (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (S76380) putative protein kinase=YCR101 [Saccharomyces cerevisiae, Peptide, 603 aa] [Saccharomyces cerevisiae] ; (X59720) YCR008w, len:603 [Saccharomyces cerevisiae] "
16506	ENU00300	ANI61C1085 45-64 7:3708..2609		1083-1102	EST	"g4c03a1.r1, g4c03a1.fl"		123	2E-27				Dynamin-like protein C12C2.08 ; (Z54140) dynamin-related protein [Schizosaccharomyces pombe]
16507	ENU00301	ANI61C9149: 27-46 1087..2190		1069-1088	EST	"m5b05a1.r1, m5b05a1.fl"		90	4E-46				(AF003835) isopenityl diphosphate:dimethylallyl diphosphate isomerase [Rattus norvegicus]
16508	ENU00302	ANI61C352:8 26-45 960..10076		1066-1100	EST	"j9e11a1.r1, j9e11a1.fl"		79	5E-14				hypothetical protein YOL071w - yeast (Saccharomyces cerevisiae) ; (Z74813) ORF YOL071w [Saccharomyces cerevisiae]
16509	ENU00303	ANI61C312:2 52-71 088..960		1106-1138	EST	"g3f04a1.r1, g3f04a1.fl"							

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16510	ENU00304	ANI61C2872: 1333..193	43-63		1122-1141	EST	"i0a05a1.r1, i0a05a1.fl"		357	9E-98				"glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae] "
16511	ENU00305	ANI61C1373: 2625..3780	69-88		1153-1182	EST	"z7b06a1.r1, z7b06a1.fl"		32	7.6				hypothetical ABC transporter ATP-binding protein CY3G12.08 ; (Z79702) hypothetical protein Rv2326c [Mycobacterium tuberculosis] dolichyl-phosphate-mannose--protein mannosyltransferase 2 ; hypothetical protein YAL023 - yeast (Saccharomyces cerevisiae) ; (L05146) Pmt2p: protein O-D-mannosyltransferase [Saccharomyces cerevisiae] ; (L05027) ORF YAL23 [Saccharomyces cerevisiae]
16512	ENU00306	ANI61C9941: 1716..542	46-65		1156-1178	EST	"h4a11a1.r1, h4a11a1.fl"		224	6E-87				"glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae] "
16513	ENU00307	ANI61C2872: 1385..193	42-64		1173-1192	EST	"c6c08a1.r1, c6c08a1.fl"		378	e-104				ORM1 protein ; probable membrane protein YGR038w - yeast (Saccharomyces cerevisiae) ; (Z72823) ORF YGR038w [Saccharomyces cerevisiae]
16514	ENU00308	ANI61C9181: 6707..5501	40-59		1182-1204	EST	"g4c08a1.r1, g4c08a1.fl"		169	3E-49				(AF047004) dimethylglycine dehydrogenase-like protein isoform 1; putative sarcosine dehydrogenase [Homo sapiens]
16515	ENU00309	ANI61C8866: 224..1436	23-42		1171-1193	EST	"k5h03a1.r1, k5h03a1.fl"		76	6E-13				splicing factor U2AF homolog - mouse ; (X64587) orf [Mus musculus]
16516	ENU00310	ANI61C6281: 155..1393	35-53		1209-1229	EST	"y6c08a1.r1, y6c08a1.fl"		169	8E-47				
16517	ENU00311	ANI61C9556: 7091..5789	29-48		1270-1289	EST	"d3d03a1.r1, d3d03a1.fl"							

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16518	ENU00312	ANI61C1004	0:1354..50	24-44	1267-1286	EST	"d3d05a1.rl, d3d05a1.fl"		120	2E-26				(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens]; (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens] probable membrane protein YPL006w - yeast (Saccharomyces cerevisiae); (Z48483) unknown [Saccharomyces cerevisiae]; (U33335) Lpa1lp [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] (AC003027) lelprt_seq No definition line found [Arabidopsis thaliana] (AF010145) hexose transporter [Aspergillus parasiticus] Spermidine synthase (putrescine aminopropyltransferase) (SPDSY); (Z54140) putrescine aminopropyltransferase [Schizosaccharomyces pombe] (AL032632) predicted using Genefinder; similar to Myosin head (motor domain); cDNA EST yk209b12.5 comes from this gene; cDNA EST yk248g5.3 comes from this gene; cDNA EST yk248g5.5 comes from this gene; cDNA EST yk398h10.3 comes...
16519	ENU00313	ANI61C7887:	32-51	1296-1317	EST		"p0h07a1.rl, p0h07a1.fl"		255	4E-67				
16520	ENU00314	ANI61C3862:	57-76	1336-1365	EST		"d4c06a1.rl, d4c06a1.fl"		212	6E-54				
16521	ENU00315	ANI61C903:1	56-73	1362-1388	EST		"o0f08a1.rl, o0f08a1.fl"		300	e-135				
16522	ENU00316	ANI61C4572:	54-73	1365-1387	EST		"h4a05a1.rl, h4a05a1.fl"		129	1E-40				
16523	ENU00317	ANI61C6258:	48-67	1364-1384	EST		"r1e10a1.rl, r1e10a1.fl"		32	7.1				
16524	ENU00318	ANI61C5156:	37-58	1375-1396	EST		"y8e05a1.rl, y8e05a1.fl"		343	2E-93				
16525	ENU00319	ANI61C2972:	51-70	1435-1463	EST		"y6f05a1.rl, y6f05a1.fl"		242	e-104				"Succinic semialdehyde dehydrogenase ; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens]; (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16526	ENU00320	ANI61C6489: 8615..7108	50-69	1482-1515	EST	"g7h07a1.r1, g7h07a1.fl"			73	2E-34			hypothetical 42.3 KD protein in YTA2-DIT1 intergenic region ; hypothetical protein YDR400w - yeast (Saccharomyces cerevisiae) ; (U32274) Ydr400wp; CAI: 0.14 [Saccharomyces cerevisiae]
16527	ENU00321	ANI61C41:22 27..705	40-60	1489-1520	EST	"i7c04a1.r1, i7c04a1.fl"			316	2E-85			glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase) ; glucosamine-6-phosphate deaminase protein (nagB) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32700) glucosamine-6-phosphate isomerase (nagB) [Haemophilus influenzae Rd]
16528	ENU00322	ANI61C5260: 516..2046	40-59	1504-1528	EST	"c4h09a1.r1, c4h09a1.fl"			347	8E-95			gamma-glutamyl phosphate reductase (GPR) (glutamate-5-semialdehyde dehydrogenase) (glutamyl-gamma-semialdehyde dehydrogenase) ; glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41) - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06155 [Saccharomyces cerevisiae] ; (U43565) gamma-glutamyl phosphate reductase [Saccharomyces cerevisiae] ; (Z75231) ORF YOR323c [Saccharomyces cerevisiae]
16529	ENU00323	ANI61C7453: 1689..3255	50-69	1555-1574	EST	"y4d12a1.r1, y4d12a1.fl"			155	5E-37			pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 ; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster] (AB000281) krev-1 [Neurospora crassa]
16530	ENU00324	ANI61C1897: 3224..1593	70-89	1635-1658	EST	"m6h05a1.r1, m6h05a1.fl"			158	9E-38			(AJ000504) Meis2a homeodomain protein [Mus musculus]
16531	ENU00325	ANI61C715:5 48..2259	70-89	1718-1737	EST	"y4b11a1.r1, y4b11a1.fl"			81	3E-14			

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16532	ENU00326	ANI61C6741: 22-41	2777..4487		1662-1690	EST	"m5f01a1.r1, m5f01a1.fl"		134	9E-37				acid protease precursor ; acid proteinase (EC 3.4.23.-) PEP1 precursor - yeast (Saccharomycopsis fibuligera) ; (D00313) open reading frame of PEP1 (putative secretable acid protease) [Saccharomycopsis fibuligera] ; acid protease PEP1 [Saccharomycopsis fibuligera]
16533	ENU00327	ANI61C7453: 50-69	1689..3454		1754-1773	EST	"g6g01a1.r1, g6g01a1.fl"		155	6E-37				pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 ; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
16534	ENU00328	ANI61C146:5 31-50	780..5675		1855-1876	EST	"m5h10a1.r1, m5h10a1.fl"		52	0.00001				(Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
16535	ENU00329	ANI61C7950: 53-72	2442..624		1937-1957	EST	"g6d12a1.r1, g6d12a1.fl"		97	5E-19				probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emicella nidulans]
16536	ENU00330	ANI61C292:5 27-46	926..8002		2037-2060	EST	"c6c10a1.r1, c6c10a1.fl"		134	3E-30				"(Z98762) SPAC4A8.06c, unknown, len:578aa, some similarity eg. to BAH_STRHY, Q01109, acetylhydrolase, (299aa), fasta sco res, opt:259, E():8.2e-17, (35.6% identity in 118 aa overl ap) [Schizosaccharomyces pombe]"
16537	ENU00331	ANI61C8138: 22-45	1813..1614		149-179	EST	"o0g08a1.r1, o0g08a1.fl"		29	3.3				(Z68879) Similarity to alcohol-steroid dehydrogenases; cDNA EST yk275a9.3 comes from this gene; cDNA EST yk275a9.5 comes from this gene [Caenorhabditis elegans] ; (Z68880) Similarity to alcohol-steroid dehydrogenases; cDNA EST yk275a9.3 comes from this gene; cDNA EST yk275a9.5 comes from this gene [Caenorhabditis elegans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16538	ENU00332	ANI61C8543: 1308..1109	32-55	167-189	EST	"g8d02a1.r1, g8d02a1.fl"			29	4.4			coenzyme PQQ synthesis protein C (coenzyme PQQ synthesis protein I); gene I protein - Acinetobacter calcoaceticus ; (X06452) gene I [Acinetobacter calcoaceticus]
16539	ENU00333	ANI61C8580: 3853..4053	27-46	158-185	EST	"c1a11a1.r1, c1a11a1.fl"							
16540	ENU00334	ANI61C6714: 4109..3905	22-48	165-184	EST	"p0b08a1.r1, p0b08a1.fl"							
16541	ENU00335	ANI61C1027 7:4906..5110	22-53	149-184	EST	"w4g12a1.r1, w4g12a1.fl"							
16542	ENU00336	ANI61C3347: 26-47 2768..2973	26-47	154-189	EST	"t2b02a1.r1, t2b02a1.fl"			28	9.7			(AF022972) similar to C. elegans olfactory receptor ODR-10 (GB:U49449) [Caenorhabditis elegans] "probable T-complex protein 1, ETA subunit (TCP-1-ETA) (CCT-ETA) ; (Z95397) Cct7p [Schizosaccharomyces pombe] "
16543	ENU00337	ANI61C1049 7:1475..1683	31-51	178-197	EST	"c9e10a1.r1, c9e10a1.fl"			66	2E-15			(AF032464) unknown [Leishmania mexicana mexicana] (Y10616) SMTA-2 protein [Sordaria macrospora] "3',5'-cyclic-nucleotide phosphodiesterase (PDEase) ; probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) pde1 - fission yeast (Schizosaccharomyces pombe) ; (S64907) Dictyostelium discoideum phosphodiesterase homolog [Schizosaccharomyces pombe=fission yeast, Peptide, 346 aa] [Schizosaccharomyces pombe] ; (AL031545) 3',5'-cyclic-nucleotide phosphodiesterase [Schizosaccharomyces pombe] ; pde1 gene [Schizosaccharomyces pombe] "
16544	ENU00338	ANI61C6193: 1220..1011	25-48	165-192	EST	"y8a10a1.r1, y8a10a1.fl"			29	5.7			"(AF016659) contains similarity to ankyrin repeats; partial CDS, this gene probably begins in the next clone [Caenorhabditis elegans] "
16545	ENU00339	ANI61C9537: 418..628	61-80	205-229	EST	"y8d05a1.r1, y8d05a1.fl"			32	0.38			
16546	ENU00340	ANI61C8199: 3060..2848	68-87	203-238	EST	"z1c08a1.r1, z1c08a1.fl"			28	7.4			
16547	ENU00341	ANI61C9708: 2531..2744	22-50	157-192	EST	"o6a04a1.r1, o6a04a1.fl"			30	1.9			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16548	ENU00342	ANI61C7957: 1675..1463	22-41	157-192	EST	"c9d07a1.rl, c9d07a1.fl"		32	0.65				(Z81050) Similarity to Shrimp amylase (TR:Q26193); cDNA EST [Caenorhabditis elegans] [Caenorhabditis elegans] carboxy-terminal proteinase (EC 3.4.21.-) prc - Escherichia coli ; (D00674) ORF of prc gene [Escherichia coli] (AJ002204) polyamine oxidase [Zea mays] (Z49073) similarity to the OV-17 antigen precursor from onchocerca volvulus (Swiss Prot accession number P36991) [Caenorhabditis elegans] (Z49073) similarity to the OV-17 antigen precursor from onchocerca volvulus (Swiss Prot accession number P36991) [Caenorhabditis elegans] DNA binding protein - Emericella nidulans ; (Z47081) DNA binding protein [Emericella nidulans] (AE001208) conserved hypothetical protein [Treponema pallidum] neutral proteinase II - Aspergillus oryzae neutral proteinase II - Aspergillus oryzae "(Y12655) 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component [Pseudomonas putida] " "growth factor-responsive protein, vascular smooth muscle - rat ; (U06713) SM-20 [Rattus norvegicus] " (Z99532) conserved hypothetical protein [Schizosaccharomyces pombe] protein-tyrosine kinase (EC 2.7.1.12) - human ; (L13738) activated p21cdc42Hs kinase [Homo sapiens] ; non-receptor Tyr kinase [Homo sapiens]
16549	ENU00343	ANI61C5524: 63-82 1497..1284	63-82	199-234	EST	"j0a01a1.rl, j0a01a1.fl"		29	4.3				
16550	ENU00344	ANI50C4357 _1:203..416	38-60	190-209	EST	"m8b11a1.rl, m8b11a1.fl"		45	0.000000	03			
16551	ENU00345	ANI61C5958: 27-47 318..105	27-47	180-199	EST	"z2f12a1.rl, z2f12a1.fl"		29	5.6				
16552	ENU00346	ANI61C5958: 29-49 318..105	29-49	182-201	EST	"s8h07a1.rl, s8h07a1.fl"		29	5.6				
16553	ENU00347	ANI61C7015: 50-70 7018..6798	50-70	209-228	EST	"c5d05a1.rl, c5d05a1.fl"		31	0.84				
16554	ENU00348	ANI61C6213: 22-44 2661..2441	22-44	165-200	EST	"o6f12a1.rl, o6f12a1.fl"		30	2.5				
16555	ENU00349	ANI61C3157: 70-89 382..578	70-89	222-249	EST	"x9f02a1.rl, x9f02a1.fl"		37	0.015				
16556	ENU00350	ANI61C3157: 70-89 382..578	70-89	222-249	EST	"x9f01a1.rl, x9f01a1.fl"		37	0.015				
16557	ENU00351	ANI61C7797: 52-72 2467..2244	52-72	211-232	EST	"x7d03a1.rl, x7d03a1.fl"		30	2.5				
16558	ENU00352	ANI61C475:1 71-90 851..2074	71-90	223-252	EST	"r1e07a1.rl, r1e07a1.fl"		30	2.3				
16559	ENU00353	ANI61C5180: 55-74 690..914	55-74	215-237	EST	"w8h01a1.rl, w8h01a1.fl"		30	3				
16560	ENU00354	ANI61C3752: 38-57 1462..1687	38-57	200-221	EST	"e4b01a1.rl, e4b01a1.fl"		31	1				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16561	ENU00355	ANI61C4777: 1066..840	38-57	193-222	EST	"h0b08a1.r1, h0b08a1.fl"			122	4E-28			"Aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans] "
16562	ENU00356	ANI61C4718: 1183..1410	22-57	187-207	EST	"r6b04a1.r1, r6b04a1.fl"		28	28	9.1			peroxisome biogenesis factor 13; peroxisomal membrane protein PEX13 (peroxin-13); (AF048755) HsPex13p [Homo sapiens]; (U71374) HsPex13p [Homo sapiens]
16563	ENU00357	ANI61C5532: 64..292	32-57	188-218	EST	"y8h06a1.r1, y8h06a1.fl"		29	29	4.1			hypothetical 16.2 KD protein in PFK1-TDS4 intergenic region; hypothetical protein YGR243w - yeast (Saccharomyces cerevisiae); (Z73028) ORF YGR243w [Saccharomyces cerevisiae]
16564	ENU00358	ANI61C971:9 74..746	22-43	188-208	EST	"x9h10a1.r1, x9h10a1.fl"		29	29	4.1			(U80842) ZC239.9 gene product [Caenorhabditis elegans]
16565	ENU00359	ANI61S4572: 1..230	22-54	185-209	EST	"r1f01a1.r1, r1f01a1.fl"		48	48	0.00001			(AL032631) predicted using Genefinder; cDNA EST yk393b10.5 comes from this gene; cDNA EST yk403h3.3 comes from this gene; cDNA EST yk403h3.5 comes from this gene; cDNA EST yk252h6.3 comes from this gene; cDNA EST yk252h6.5 come...
16566	ENU00360	ANI61C1083 4-2471..2242	39-58	195-226	EST	"q0a10a1.r1, q0a10a1.fl"		43	43	0.0003			(D87063) chitinase [Emericella nidulans]
16567	ENU00361	ANI61C4987: 777..545	22-49	184-212	EST	"o8h01a1.r1, o8h01a1.fl"		31	31	1.9			(AF026401) stearyl-CoA desaturase [Mucor rouxii]
16568	ENU00362	ANI61C5234: 844..1078	23-49	188-215	EST	"a0a05a1.r1, a0a05a1.fl"		30	30	3.3			gene hb protein - mouse (fragment); (X81634) hb [Mus musculus]
16569	ENU00363	ANI61C6800: 1284..1050	30-50	191-222	EST	"i3b03a1.r1, i3b03a1.fl"		32	32	0.5			"(AE001069) molybdopterin oxidoreductase, iron-sulfur binding subunit [Archaeoglobus fulgidus] "

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16570	ENU00364	ANI61C1364: 237..1	72-92	231-265	EST	"x9d10a1.rl, x9d10a1.fl"			29	5.9			"alpha-amylase type B isozyme precursor (1,4-alpha-D-glucan glucanOhydrolase) (clones GRAMY56 and 963) ; alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley ; (X15227) alpha amylase [Hordeum vulgare] ; high pl alpha amylase [Hordeum vulgare var. distichum] "
16571	ENU00365	ANI61C3918: 3045..3280	23-52	186-216	EST	"y8c02a1.rl, y8c02a1.fl"			29	4.5			"triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - dog ; (M35302) lipase precursor [Canis familiaris] "
16572	ENU00366	ANI61C1028 0:110..347	27-46	196-222	EST	"r2g06a1.rl, r2g06a1.fl"			31	1.2			Conidiation-specific protein 10; Neurospora crassa ; (M20005) conidiation-specific protein con-10 [Neurospora crassa]
16573	ENU00367	ANI61C1968: 611..372	65-84	233-262	EST	"m8a09a1.rl, m8a09a1.fl"			32	0.54			(AF038948) ultraviolet cone visual pigment; rhodopsin [Ambystoma tigrinum]
16574	ENU00368	ANI61C5343: 767..526	48-69	217-247	EST	"o9h08a1.rl, o9h08a1.fl"			64	1E-10			(AF093244) import protein Tim9p [Saccharomyces cerevisiae]
16575	ENU00369	ANI61C5354: 9..251	30-53	199-230	EST	"g9f01a1.rl, g9f01a1.fl"			29	4.8			(Z46276) Ig heavy chain variable region [Homo sapiens]
16576	ENU00370	ANI61C2518: 513..270	22-41	196-223	EST	"m6b02a1.rl, m6b02a1.fl"			31	2.3			(X98456) ORF 2 [Mus musculus]
16577	ENU00371	ANI61C8695: 4642..4889	29-55	210-234	EST	"r4c07a1.rl, r4c07a1.fl"			31	2.4			(AC000132) Strong similarity to Dianthus cysteine proteinase (gb U17135). [Arabidopsis thaliana]
16578	ENU00372	ANI61C1147 7:1040..790	47-66	236-255	EST	"c9e12a1.rl, c9e12a1.fl"							
16579	ENU00373	ANI61C7858: 2004..1752	47-66	234-257	EST	"m0c05a1.rl, m0c05a1.fl"							
16580	ENU00374	ANI61C6863: 1064..805	27-49	225-244	EST	"j0c04a1.rl, j0c04a1.fl"							
16581	ENU00375	ANI61C1748: 899..1158	31-53	217-248	EST	"y6c05a1.rl, y6c05a1.fl"							
16582	ENU00376	ANI61C4718: 1143..1410	35-70	240-260	EST	"x5f07a1.rl, x5f07a1.fl"							
16583	ENU00377	ANI61C1626: 1305..1037	22-52	229-248	EST	"r5a02a1.rl, r5a02a1.fl"							

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16584	ENU00378	ANI61C1253: 6182..6451	58-77	261-285	EST	"c9d06a1.rl, c9d06a1.fl"				31	1.6			UL52 [Bovine herpesvirus 1] ; (AJ004801) component of DNA helicase/primase complex [Bovine herpesvirus type 1.1]
16585	ENU00379	ANI61C9672: 3072..2798	22-55	234-254	EST	"dlg10a1.rl, dlgl0a1.fl"				34	0.26			S59/4 homeotic protein - fruit fly (Drosophila melanogaster)
16586	ENU00380	ANI61C5697: 279..1	48-67	262-284	EST	"r5b08a1.rl, r5b08a1.fl"				31	2.2			(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]
16587	ENU00381	ANI61C9139: 688..410	55-77	264-291	EST	"z1f06a1.rl, z1f06a1.fl"				30	3.8			"(AL034559) predicted using hexExon; MAL3P7.37 (PFC1030w), Hypothetical protein, len: 1543 aa [Plasmodium falciparum] "
16588	ENU00382	ANI61C2195: 296..17	33-51	241-270	EST	"m8h11a1.rl, m8h11a1.fl"				69	6E-12			(AL023635) hypothetical protein MLCB1243.36 [Mycobacterium leprae]
16589	ENU00383	ANI61C1049 0:1251..1532	23-50	243-262	EST	"g6g03a1.rl, g6g03a1.fl"				31	1.7			cryptogene protein G4 - Sauroleishmania tarentolae (strain LEM125)
16590	ENU00384	ANI61C1029 6:4459..4741	22-56	236-262	EST	"i0h11a1.rl, i0h11a1.fl"				33	0.63			(AJ000871) histidine kinase [Streptococcus mitis]
16591	ENU00385	ANI61C7052: 3030..2741	48-74	262-295	EST	"g9g11a1.rl, g9g11a1.fl"				68	2E-11			PMP47A ; 47K peroxisomal membrane protein - yeast (Candida boidinii) ; (J05672) peroxisomal membrane protein [Candida boidinii]
16592	ENU00386	ANI61C1754: 347..639	22-54	246-272	EST	"y6h08a1.rl, y6h08a1.fl"				30	4.4			(AB003699) Cdc7-related kinase [Xenopus laevis]
16593	ENU00387	ANI61C7776: 3863..3567	45-66	274-299	EST	"h0h05a1.rl, h0h05a1.fl"				37	0.034			(Z99292) hypothetical protein [Schizosaccharomyces pombe]
16594	ENU00388	ANI61C319:4 907..5205	22-45	258-277	EST	"m8a02a1.rl, m8a02a1.fl"								
16595	ENU00389	ANI61C8590: 194..494	37-58	268-295	EST	"c5e10a1.rl, c5e10a1.fl"								
16596	ENU00390	ANI61C1017 1:2998..2696	22-41	257-282	EST	"y8g02a1.rl, y8g02a1.fl"								
16597	ENU00391	ANI61C1049 0:1227..1532	22-54	266-285	EST	"o8f10a1.rl, o8f10a1.fl"				69	7E-12			(AL023635) hypothetical protein MLCB1243.36 [Mycobacterium leprae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16598	ENU00392	ANI61C8580: 7053..7358	49-67	293-312	EST	"i0e02a1.rl, i0e02a1.fl"			31	3.5			glucose inhibited division protein B ; (U97573) gidB homolog [Treponema pallidum] ; (AE001263) glucose-inhibited division protein B (gidB) [Treponema pallidum] probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16599	ENU00393	ANI61C7799: 9..315	27-46	256-291	EST	"n3a07a1.rl, n3a07a1.fl"			31	2.1			probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16600	ENU00394	ANI61C9506: 1881..1574	32-52	267-297	EST	"y6e07a1.rl, y6e07a1.fl"							
16601	ENU00395	ANI61C7799: 9..316	27-46	257-292	EST	"e9a07a1.rl, e9a07a1.fl"			31	2.1			probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16602	ENU00396	ANI61C9506: 1881..1574	32-52	267-297	EST	"l3b06a1.rl, l3b06a1.fl"							
16603	ENU00397	ANI61C1453: 283..592	54-73	295-321	EST	"b0h04a1.rl, b0h04a1.fl"							
16604	ENU00398	ANI61C4718: 1101..1410	23-45	270-290	EST	"o6h06a1.rl, o6h06a1.fl"							
16605	ENU00399	ANI61C6956: 3451..3765	24-43	275-296	EST	"m5f11a1.rl, m5f11a1.fl"			29	8.4			"cytochrome P450 52C2 (CYPL1C2) (alkane-inducible P450-ALK6-A) ; cytochrome P450 ALK6-A, alkane-inducible - yeast (Candida maltosa) ; (D12718) n-alkane inducible cytochrome P-450 [Candida maltosa] " (AE000820) magnesium chelatase subunit [Methanobacterium thermoautotrophicum] probable clathrin heavy chain ; (Z69240) clathrin heavy chain [Schizosaccharomyces pombe]
16606	ENU00400	ANI61C692:4 92..173	22-55	274-299	EST	"x7g04a1.rl, x7g04a1.fl"			30	5.1			
16607	ENU00401	ANI61C2935: 550..231	43-62	290-320	EST	"w4e09a1.rl, w4e09a1.fl"			46	0.00006			
16608	ENU00402	ANI61C9040: 1556..1876	22-56	265-300	EST	"o0b07a1.rl, o0b07a1.fl"							
16609	ENU00403	ANI61C124:1 235..909	24-47	280-308	EST	"y4a12a1.rl, y4a12a1.fl"			31	2.3			(D49697) 106.4KD protein [Nilaparvata lugens reovirus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16610	ENU00404	ANI61C6709: 644..314	36-56	290-324	EST	"k5e05a1.rl, k5e05a1.fl"			31	3.1			zinc finger protein MSN4 (multicopy suppressor of SNF1 protein 4) ; finger protein MSN4 - yeast (Saccharomyces cerevisiae) ; (L08839) zinc finger protein [Saccharomyces cerevisiae] ; (X75781) human transcription factor homologue [Saccharomyces cerevisiae] ; (Z28062) ORF YKL062w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
16611	ENU00405	ANI61C6046: 1179..848	22-52	290-311	EST	"clb10a1.rl, clb10a1.fl"		32		1.1			hypothetical 12.8 KD protein in ARO9-SPS100 intergenic region precursor ; hypothetical protein YHR138c - yeast (Saccharomyces cerevisiae) ; (U10398) Yhr138cp [Saccharomyces cerevisiae] ; (Y13625) hypothetical protein [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AF066054) formaldehyde dehydrogenase [Pichia pastoris]
16612	ENU00406	ANI61C7955: 405..73	31-49	301-321	EST	"h4c10a1.rl, h4c10a1.fl"		112		5E-35			Intercellular adhesion molecule-1 precursor (ICAM-1) ; (U65789) intercellular adhesion molecule-1 [Bos taurus]
16613	ENU00407	ANI61C1112 9:889..563	22-42	287-313	EST	"m0h06a1.rl, m0h06a1.fl"		32		1.4			(U42845) coded for by C. elegans cDNA yk63a8.5; coded for by C. elegans cDNA yk83a12.5; coded for by C. elegans cDNA yk74b10.5; coded for by C. elegans cDNA yk64a6.5; coded for by C. elegans cDNA yk108g8.5; coded for by C. elegans cDNA yk90b... exodeoxyribonuclease V (EC 3.1.1.5) 67K chain - Escherichia coli ; (X04582) exonuclease V alpha subunit (AA 1-608) [Escherichia coli] (AJ005589) protein tyrosine phosphatase [Pisum sativum] (U74668) soluble transducer protein HtH [Halobacterium salinarum]
16614	ENU00408	ANI61C1029 0:98..433	22-56	287-315	EST	"z3d09a1.rl, z3d09a1.fl"		67		9E-21			
16615	ENU00409	ANI61C9613: 533..872	25-45	300-322	EST	"clh09a1.rl, clh09a1.fl"		32		1.9			
16616	ENU00410	ANI61C2251: 777..1118	50-69	327-349	EST	"z4h11a1.rl, z4h11a1.fl"		36		0.075			
16617	ENU00411	ANI61C3279: 568..227	31-50	298-330	EST	"o1f04a1.rl, o1f04a1.fl"		31		2.5			
16618	ENU00412	ANI61C6812: 4365..4708	39-60	313-340	EST	"q0c10a1.rl, q0c10a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16619	ENU00413	ANI61C6812: 4365..4708	36-57	310-337	EST	"o9c11a1.rl, o9c11a1.fl"			31	2.5			(U74668) soluble transducer protein Hth [Halobacterium salinarum]
16620	ENU00414	ANI61C6812: 4365..4708	26-47	300-327	EST	"g6a05a1.rl, g6a05a1.fl"			31	2.5			(U74668) soluble transducer protein Hth [Halobacterium salinarum]
16621	ENU00415	ANI61C2656: 1399..1505	40-59	312-343	EST	"f0h06a1.rl, f0h06a1.fl"			31	4.3			TBF1 protein (TTAGGG repeat-binding factor 1) (TBF alpha) ; TTAGGG repeat-binding factor 1 - yeast (Saccharomyces cerevisiae) ; (U43703) Tbf1p [Saccharomyces cerevisiae]
16622	ENU00416	ANI61C6003: 398..743	65-85	349-368	EST	"b0g08a1.rl, b0g08a1.fl"			29	9.8			(U33940) gp46 surface membrane protein [Simian T-cell lymphotropic virus type 1]
16623	ENU00417	ANI61C2752: 589..243	54-73	339-358	EST	"o8b12a1.rl, o8b12a1.fl"			222	6E-58			CATALase B ; (U80672) catalase [Emicella nidulans]
16624	ENU00418	ANI61C9663: 2057..2403	25-59	298-329	EST	"w8e04a1.rl, w8e04a1.fl"			34	0.39			(U16751) cold-responsive gene product [Brassica oleracea]
16625	ENU00419	ANI61C2968: 909..563	23-56	295-327	EST	"m7e04a1.rl, m7e04a1.fl"			59	0.000000	02		"mitochondrial 60S ribosomal protein L24 precursor (YML24) ; ribosomal protein Yml24, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z47815) ribosomal protein [Saccharomyces cerevisiae]"
16626	ENU00420	ANI61C1731: 468..114	72-94	350-384	EST	"e0d10a1.rl, e0d10a1.fl"			89	2E-17			Conidium-specific protein ; SpoC1-C1D protein - Emicella nidulans ; (X54668) SpoC1-C1D product [Emicella nidulans]
16627	ENU00421	ANI61C7024: 407..762	55-74	336-368	EST	"q0e11a1.rl, q0e11a1.fl"			35	0.24			amidase (EC 3.5.1.4) - Aspergillus oryzae ; (D10492) acetamidase [Aspergillus oryzae]
16628	ENU00422	ANI61C4014: 1146..790	35-54	330-349	EST	"y8c04a1.rl, y8c04a1.fl"			32	1.2			(U81825) pacifastin light chain precursor [Pacifastacus leniusculus]
16629	ENU00423	ANI61C713: 337..1976	45-64	330-364	EST	"z1g01a1.rl, z1g01a1.fl"			30	6.2			tyrA protein - Bacillus subtilis ; (M80245) TyrA [Bacillus subtilis] ; (Z99115) prephenate dehydrogenase [Bacillus subtilis]
16630	ENU00424	ANI61C3305: 1206..842	22-53	325-344	EST	"r7d11a1.rl, r7d11a1.fl"			30	8.3			mucin JER57 - human
16631	ENU00425	ANI61C3024: 1315..1680	26-46	321-349	EST	"y6e02a1.rl, y6e02a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16632	ENU00426	ANI61C9488: 629..263	22-47	314-346	EST	"c8e02a1.rl, c8e02a1.fl"		68	2E-11				(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea] (AF049107) response regulator homolog [Mycococcus xanthus] (AL021426) cwIM [Mycobacterium tuberculosis] probable membrane protein YOL089c - yeast (Saccharomyces cerevisiae) ; (X83121) orf 00938 [Saccharomyces cerevisiae] ; (Z74831) ORF YOL089c [Saccharomyces cerevisiae]
16633	ENU00427	ANI61C7171: 2045..2412	70-89	368-395	EST	"y8g06a1.rl, y8g06a1.fl"		33	0.74				
16634	ENU00428	ANI61C1077 3:2911..2542	70-89	370-397	EST	"j0g10a1.rl, j0g10a1.fl"		31	4.9				
16635	ENU00429	ANI61C1105 4:1301..1670	31-58	334-358	EST	"c6a01a1.rl, c6a01a1.fl"		39	0.01				
16636	ENU00430	ANI61C5376: 329..700	45-64	345-374	EST	"o8h06a1.rl, o8h06a1.fl"		36	0.15				metallothionein-like protein 1 ; metallothionein - barley ; (X58540) ids-1 [Hordeum vulgare]
16637	ENU00431	ANI61C9746: 4418..4047	71-91	372-400	EST	"z4h04a1.rl, z4h04a1.fl"		33	1				(AF071059) zinc finger RNA binding protein [Mus musculus]
16638	ENU00432	ANI61C5649: 145..519	24-53	329-356	EST	"l0a09a1.rl, l0a09a1.fl"		30	8.8				hypothetical 49.6 KD protein in OMPP 3'region precursor ; (X74278) ORF [Escherichia coli]
16639	ENU00433	ANI61C5657: 755..379	22-49	334-356	EST	"c4f12a1.rl, c4f12a1.fl"		30	8.8				hypothetical 49.6 KD protein in OMPP 3'region precursor ; (X74278) ORF [Escherichia coli]
16640	ENU00434	ANI61C9902: 2140..2517	22-45	331-357	EST	"g6d04a1.rl, g6d04a1.fl"		30	8.8				hypothetical protein HHRF4 ; HHRF4 protein - human cytomegalovirus (strain AD169) ; (X04650) HHRF4 reading frame [human herpesvirus 5] ; (X17403) HCMVUS29 [human herpesvirus 5]
16641	ENU00435	ANI61C9902: 2140..2517	22-45	331-357	EST	"x8d07a1.rl, x8d07a1.fl"		32	2.3				transcription factor SL1 - human ; (L39059) transcription factor SL1 [Homo sapiens]
16642	ENU00436	ANI61C7527: 444..66	22-51	336-358	EST	"c8g08a1.rl, c8g08a1.fl"		35	0.21				
16643	ENU00437	ANI61C9007: 1132..752	72-91	375-410	EST	"flb11a1.rl, flb11a1.fl"							
16644	ENU00438	ANI61C5627: 3687..3307	50-69	353-388	EST	"i0d03a1.rl, i0d03a1.fl"							
16645	ENU00439	ANI61C8042: 22..404	43-61	350-383	EST	"o8a10a1.rl, o8a10a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16646	ENU00440	ANI61C5175: 3158..3541	23-47	343-363	EST	"y6a11a1.r1, y6a11a1.fl"			32	2.3			"Erythronolide synthase, modules 1 and 2 (ORF 1) (6-deoxyerythronolide B synthase I) (DEBS 1) " (L04667) resolvase [Plasmid RP4]
16647	ENU00441	ANI61C440:4 20..36	28-47	350-370	EST	"w4f08a1.r1, w4f08a1.fl"		30	9				M polyprotein - Rift Valley fever virus (strain ZH-501)
16648	ENU00442	ANI61C7649: 131..297	69-90	383-415	EST	"r4a02a1.r1, r4a02a1.fl"		32	1.4				(AL023634) hypothetical protein [Schizosaccharomyces pombe]; (AF095790) BAG-family molecular chaperone regulator-1B protein [Schizosaccharomyces pombe]
16649	ENU00443	ANI61C1012 2:2192..1803	22-47	344-369	EST	"g6b06a1.r1, g6b06a1.fl"		41	0.005				(AF052832) unknown [Trypanosoma cruzi]
16650	ENU00444	ANI61C1109 0:2478..2084	65-84	382-417	EST	"z3e08a1.r1, z3e08a1.fl"		34	0.64				ribosomal protein S14.e - Neurospora crassa
16651	ENU00445	ANI61C3946: 2627..3024	35-54	356-390	EST	"g6c04a1.r1, g6c04a1.fl"		55	4E-18				(U43840) GmCK3p [Glycine max]
16652	ENU00446	ANI61C3084: 180..577	58-80	392-413	EST	"y4f05a1.r1, y4f05a1.fl"		41	0.003				(D90910) hypothetical protein [Synechocystis sp.]
16653	ENU00447	ANI61C1141 3:144..542	57-76	378-413	EST	"r2h05a1.r1, r2h05a1.fl"		39	0.011				voltage-gated potassium channel protein KV1.1 (MK1) (MBK1); potassium channel KV1.1 protein - mouse; (Y00305) potassium channel protein-1 (AA 1-495) [Mus musculus]; (M30439) potassium channel protein [Mus musculus]; K channel protein [Mus musculus]
16654	ENU00448	ANI61C3310: 503..103	71-90	410-429	EST	"g8a03a1.r1, g8a03a1.fl"		32	2.5				(U66846) orf5 [Streptococcus pneumoniae]
16655	ENU00449	ANI61C2937: 761..1161	22-54	356-380	EST	"h1b05a1.r1, h1b05a1.fl"		30	9.7				(AB011167) KIAA0595 protein [Homo sapiens]
16656	ENU00450	ANI61C1754: 2139..1738	32-51	367-391	EST	"y8g09a1.r1, y8g09a1.fl"		30	9.8				(U48796) taxadiene synthase [Taxus brevifolia]; taxadiene synthase [Taxus brevifolia]
16657	ENU00451	ANI61C8200: 3379..2978	55-74	385-414	EST	"c8f08a1.r1, c8f08a1.fl"		31	3.3				(U65312) RNA-dependent RNA polymerase [Avian pneumovirus]
16658	ENU00452	ANI61C3381: 758..1161	51-70	377-412	EST	"a0a01a1.r1, a0a01a1.fl"							
16659	ENU00453	ANI61C261:2 090..2494	29-48	362-390	EST	"r5g10a1.r1, r5g10a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16660	ENU00454	ANI61C185:9 78..1380	36-55	377-397	EST	"k5c02a1.r1, k5c02a1.fl"			55	0.000000 004			cyclophilin-like protein wis2 - fission yeast (Schizosaccharomyces pombe) ; (X91981) wis2 [Schizosaccharomyces pombe] ; (Z98598) probable 40 kd peptidyl-prolyl cis-trans isomera se [Schizosaccharomyces pombe] (L05903) major surface glycoprotein [Pneumocystis carinii]
16661	ENU00455	ANI61C9244: 3735..4139	71-100	414-433	EST	"f2a10a1.r1, f2a10a1.fl"			31	5.7			
16662	ENU00456	ANI61C2518: 680..270	22-49	363-390	EST	"m8d03a1.r1, m8d03a1.fl"			90	9E-18			ENP1 protein ; hypothetical protein YBR247c - yeast (Saccharomyces cerevisiae) ; (Z36116) ORF YBR247c [Saccharomyces cerevisiae] ; (U50779) Enp1p [Saccharomyces cerevisiae] (AC006592) unknown protein [Arabidopsis thaliana] "(U23782) orf3; partial hypothetical protein, similar to the 55.2 kDa hypothetical protein in the HXT8 5' region of Saccharomyces cerevisiae, Swiss-Prot Accession Number P39976 [Neisseria meningitidis] "
16664	ENU00458	ANI61C6691: 1754..2166	37-60	388-407	EST	"g7a08a1.r1, g7a08a1.fl"			32	1.5			
16665	ENU00459	ANI61C9739: 7766..8182	22-53	362-396	EST	"g6a06a1.r1, g6a06a1.fl"			30	7.9			
16666	ENU00460	ANI61C9037: 539..121	61-81	418-437	EST	"z4h06a1.r1, z4h06a1.fl"			32	2			hypothetical 104.8 KD protein in CTK3-COQ5 intergenic region ; hypothetical protein YML111w - yeast (Saccharomyces cerevisiae) ; (Z49210) unknown [Saccharomyces cerevisiae] hypothetical protein KIAA0391 ; (AB002389) KIAA0391 [Homo sapiens]
16667	ENU00461	ANI61C6251: 1016..598	23-43	370-399	EST	"r5e10a1.r1, r5e10a1.fl"			30	7.8			membrane glycoprotein CLA-1 protein long form precursor - human ; (Z22555) CLA-1 [Homo sapiens] (AC004877) sco-spondin-mucin-like; similar to P98167 (PID:g1711548); details of intron/exon structure uncertain [Homo sapiens] (U00055) R02F2.8 gene product [Caenorhabditis elegans]
16668	ENU00462	ANI61C1904: 223..642	22-48	380-399	EST	"n3b03a1.r1, n3b03a1.fl"			31	6			
16669	ENU00463	ANI61C9741: 1156..1576	44-63	403-422	EST	"h1c11a1.r1, h1c11a1.fl"			32	2.7			
16670	ENU00464	ANI61C9676: 1902..2323	72-91	422-451	EST	"z3e05a1.r1, z3e05a1.fl"			31	3.5			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16681	ENU00475	ANI61C1079 9:807..361	55-76	435-459	EST	"r2f01a1.r1, r2f01a1.fl"			30	8.6			(U08029) NADH:nitrate reductase [Spinacia oleracea]
16682	ENU00476	ANI61C5287: 59-78 2720..2270	59-78	444-467	EST	"x7h08a1.r1, x7h08a1.fl"			104	3E-22			"6-phosphofructo-2-kinase 1 (phosphofructokinase 2 I) (6PF-2-K 1) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae) ; (Z38125) len: 827, CAl: 0.17, A41136 A41136; 6-phosphofructo-2-kinase [Saccharomyces cerevisiae]"
16683	ENU00477	ANI61C5287: 59-78 2720..2270	59-78	444-467	EST	"m8ell1a1.r1, m8ell1a1.fl"			104	3E-22			"6-phosphofructo-2-kinase 1 (phosphofructokinase 2 I) (6PF-2-K 1) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae) ; (Z38125) len: 827, CAl: 0.17, A41136 A41136; 6-phosphofructo-2-kinase [Saccharomyces cerevisiae]"
16684	ENU00478	ANI61C4063: 72-94 250..702	72-94	461-482	EST	"y4d05a1.r1, y4d05a1.fl"			68	3E-11			[Saccharomyces cerevisiae]" hypothetical 102.5 KD protein in KRE1-HXT14 intergenic region ; probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae) ; (Z46259) NO339 [Saccharomyces cerevisiae] ; (Z71597) ORF YNL321w [Saccharomyces cerevisiae]
16685	ENU00479	ANI61C946:1 27-46 124..1576	27-46	412-437	EST	"d5g05a1.r1, d5g05a1.fl"			34	0.59			[AF091234] putative transcription factor [Mus musculus]
16686	ENU00480	ANI61C1054 69-88 8:1251..799	69-88	460-480	EST	"x7a06a1.r1, x7a06a1.fl"			148	6E-61			(X98931) heat shock protein 70 [Emicella nidulans]
16687	ENU00481	ANI61C1253: 28-48 1..401	28-48	422-440	EST	"c4a10a1.r1, c4a10a1.fl"			33	1			(AC004684) myb-related protein [Arabidopsis thaliana]
16688	ENU00482	ANI61C6228: 22-43 495..37	22-43	407-437	EST	"i3h05a1.r1, i3h05a1.fl"			121	3E-27			(AL035064) caax prenyl protease 2 [Schizosaccharomyces pombe]
16689	ENU00483	ANI61C8193: 22-41 1030..1490	22-41	421-440	EST	"w4a11a1.r1, w4a11a1.fl"			32	2.4			(U41063) P-type ATPase [Tetrahymena thermophila]
16690	ENU00484	ANI61C9369: 22-55 848..1040	22-55	416-441	EST	"h4b05a1.r1, h4b05a1.fl"			31	5.3			(L20099) envelope glycoprotein [Simian immunodeficiency virus]
16691	ENU00485	ANI61C4221: 35-58 882..420	35-58	420-455	EST	"g5h02a1.r1, g5h02a1.fl"							
16692	ENU00486	ANI61C3695: 23-50 1088..1552	23-50	426-445	EST	"x8d02a1.r1, x8d02a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16698	ENU00492	ANI61C766:1 726..2199	48-67	454-479	EST	"j7g09a1.r1, j7g09a1.fl"			134	3E-31			"40S ribosomal protein S24E (RP50) ; ribosomal protein S24.e - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 135, CAl: 0.76, similar to RS24_HUMAN P16632 40S ribosomal protein S24 (S19) [Saccharomyces cerevisiae] ; (U18814) Rps24eap: 40S ribosomal protein S24E (RP50) [Saccharomyces cerevisiae]"
16699	ENU00493	ANI61C766:1 726..2199	48-67	454-479	EST	"c8c03a1.r1, c8c03a1.fl"			134	3E-31			"40S ribosomal protein S24E (RP50) ; ribosomal protein S24.e - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 135, CAl: 0.76, similar to RS24_HUMAN P16632 40S ribosomal protein S24 (S19) [Saccharomyces cerevisiae] ; (U18814) Rps24eap: 40S ribosomal protein S24E (RP50) [Saccharomyces cerevisiae]"
16700	ENU00494	ANI61C7522: 4086..3612	24-46	437-456	EST	"h1b06a1.r1, h1b06a1.fl"			36	0.16			(D28529) protein tyrosine phosphatase DPZPTP [Mus musculus]
16701	ENU00495	ANI61C3801: 85..559	72-100	473-504	EST	"p0d11a1.r1, p0d11a1.fl"			125	2E-28			rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
16702	ENU00496	ANI61C7089: 1..475	22-43	421-454	EST	"y8b04a1.r1, y8b04a1.fl"			32	1.9			nodulation protein NOLB ; nolB protein - Rhizobium fredii ; (L12251) nodulation protein [Rhizobium fredii]
16703	ENU00497	ANI61C7891: 516..41	52-71	458-485	EST	"h1c04a1.r1, h1c04a1.fl"							
16704	ENU00498	ANI61C1557: 6717..6239	27-62	430-463	EST	"r4a11a1.r1, r4a11a1.fl"			203	5E-52			"carbamoyl-phosphate synthase, arginine-specific, small chain precursor (arginine-specific carbamoyl-phosphate synthetase, glutamine chain) (CPS-A) ; (AF001029) carbamoyl phosphate synthetase, small subunit [Trichoderma virens]"
16705	ENU00499	ANI61C2811: 64..542	70-90	482-506	EST	"d3g03a1.r1, d3g03a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16706	ENU00500	ANI61C1128 2:645..166	22-47	440-459	EST	"f0c08a1.rl, f0c08a1.fl"			56	0.000000			(U44750) NAD-dependent 15-hydroxyprostaglandin dehydrogenase [Rattus norvegicus] (AF034606) chordin [Danio rerio]
16707	ENU00501	ANI61C3972: 2125..1642	22-52	428-463	EST	"i7c08a1.rl, i7c08a1.fl"			33	1.1			acetyl-coenzyme A synthetase (acetate-CoA ligase) (acyl-activating enzyme) ; acetate--CoA ligase (EC 6.2.1.1) - Emericella nidulans ; (X16990) acetate--CoA ligase [Emericella nidulans]
16708	ENU00502	ANI61C3878: 538..51	41-60	458-486	EST	"p0e01a1.rl, p0e01a1.fl"			196	8E-50			
16709	ENU00503	ANI61C1479: 1993..2483	22-49	448-470	EST	"i0d02a1.rl, i0d02a1.fl"			56	0.000000			(AC007109) unknown protein [Arabidopsis thaliana]
16710	ENU00504	ANI61C9694: 2425..1935	54-73	477-502	EST	"y4c12a1.rl, y4c12a1.fl"			36	0.17			(AF006492) FOG [Mus musculus]
16711	ENU00505	ANI61C9253: 4183..4061	22-46	439-471	EST	"h8g04a1.rl, h8g04a1.fl"							
16712	ENU00506	ANI61C8431: 367..861	29-50	459-481	EST	"m5b08a1.rl, m5b08a1.fl"			102	5E-25			probable chorismate mutase (CM) ; (Z98529) putative chorismate mutase [Schizosaccharomyces pombe]
16713	ENU00507	ANI61C4749: 235..730	25-52	459-478	EST	"c4e09a1.rl, c4e09a1.fl"			43	0.001			MSF1 protein ; MSF1 protein - yeast (Saccharomyces cerevisiae) ; (X70279) MSF1 protein [Saccharomyces cerevisiae] ; (U17246) Msf1p' [Saccharomyces cerevisiae]
16714	ENU00508	ANI61C1132 4:497..1	22-54	448-476	EST	"f0g05a1.rl, f0g05a1.fl"							
16715	ENU00509	ANI61C1051 7:1114..1182	48-67	483-505	EST	"m5d02a1.rl, m5d02a1.fl"			34	0.53			(AF139463) early growth response 2 protein [Homo sapiens]
16716	ENU00510	ANI61C1094 9:1013..514	39-58	477-496	EST	"o8g03a1.rl, o8g03a1.fl"			31	4.6			(U87864) neutralized homolog [Homo sapiens] ; (AF029729) neutralized [Homo sapiens]
16717	ENU00511	ANI61C3429: 797..294	55-74	484-516	EST	"h1a12a1.rl, h1a12a1.fl"							[Homo sapiens]
16718	ENU00512	ANI61C941:6 07..1111	27-48	454-489	EST	"a0b04a1.rl, a0b04a1.fl"			32	3.5			(AL021841) PE_PGRS [Mycobacterium tuberculosis]
16719	ENU00513	ANI61C5252: 1549..1045	23-52	452-485	EST	"j4d06a1.rl, j4d06a1.fl"			85	3E-16			(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi]

Accession Comparison

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16720	ENU00514	ANI61C8314: 1118..1625	36-57	482-501	EST	"r5a05a1.r1, r5a05a1.fl"			34	0.54			DNA damage tolerance protein RAD31 ; (Y08805) rad31 [Schizosaccharomyces pombe] ; (Z98560) superoxide dismutase [Schizosaccharomyces pombe] (AE001403) predicted secreted protein [Plasmodium falciparum] (D89782) thymidylate synthetase [Theileria sp.] (M77661) putative pol polyprotein [Magnaporthe grisea] (AF035770) ribosomal protein L37 [Schistosoma mansoni]
16721	ENU00515	ANI61C3915: 513..1	32-52	473-502	EST	"w4a01a1.r1, w4a01a1.fl"			31	6.2			
16722	ENU00516	ANI61C1099 8:3077..3589	42-61	477-512	EST	"z3f05a1.r1, z3f05a1.fl"			31	8.1			
16723	ENU00517	ANI61C5345: 70..585	39-59	479-512	EST	"d3c04a1.r1, d3c04a1.fl"			31	4.8			
16724	ENU00518	ANI61C3288: 3396..2881	35-54	489-508	EST	"l3e05a1.r1, l3e05a1.fl"			63	1E-17			
16725	ENU00519	ANI61C4412: 2074..2592	22-43	476-498	EST	"s9c09a1.r1, s9c09a1.fl"			43	0.001			larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis) ; glue protein lgp-1 - fruit fly (Drosophila virilis) ; (X76203) major larval glue protein [Drosophila virilis] ; (Z29565) glue protein [Drosophila virilis] ; glue protein [Drosophila virilis] hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mrs11p [Saccharomyces cerevisiae] ; (U10555) Mrs11p [Saccharomyces cerevisiae] hypothetical 23.1 KD protein in BSAA-ILVD intergenic region ; (L77246) putative [Bacillus subtilis] ; (Z99115) similar to hypothetical proteins [Bacillus subtilis] transcription factor shm - fruit fly (Drosophila melanogaster)
16726	ENU00520	ANI61C4714: 41..565	23-48	484-505	EST	"q0d03a1.r1, q0d03a1.fl"							
16727	ENU00521	ANI61C9255: 158..685	57-86	523-542	EST	"s9b03a1.r1, s9b03a1.fl"			87	1E-16			
16728	ENU00522	ANI61C6137: 3737..4265	37-55	504-523	EST	"i8c05a1.r1, i8c05a1.fl"			64	2E-17			
16729	ENU00523	ANI61C1372: 1269..738	70-89	528-559	EST	"r7g08a1.r1, r7g08a1.fl"			80	8E-15			
16730	ENU00524	ANI61C1114: 2012..2544	70-89	537-560	EST	"k0b01a1.r1, k0b01a1.fl"			34	0.58			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16731	ENU00525	ANI61C5175: 684..164	32-61	500-522	EST	"n8d07a1.r1, n8d07a1.fl"			70	9E-12			(Z82286) predicted using Genefinder [Caenorhabditis elegans]
16732	ENU00526	ANI61C1010: 58-79	527-550	504-530	EST	"h0g08a1.r1, h0g08a1.fl"			34	0.58			(U39645) repeated leucine-rich (LRR) [Caenorhabditis elegans]
16733	ENU00527	ANI61C8798: 1288..749	33-54	501-520	EST	"j9a11a1.r1, j9a11a1.fl"			66	2E-10			(AL035602) putative protein [Arabidopsis thaliana]
16734	ENU00528	ANI61C5214: 1839..2379	22-48	501-520	EST	"g9f09a1.r1, g9f09a1.fl"			31	5.1			(AE000524) carboxynorspermidine decarboxylase (nspC) [Helicobacter pylori 26695]
16735	ENU00529	ANI61C8429: 1285..743	22-42	492-522	EST	"o0h06a1.r1, o0h06a1.fl"			43	0.002			hypothetical protein YOR297c - yeast (Saccharomyces cerevisiae) ; (Z75205) ORF YOR297c [Saccharomyces cerevisiae]
16736	ENU00530	ANI61C7324: 6273..5731	72-95	546-572	EST	"h0h11a1.r1, h0h11a1.fl"			43	0.002			hypothetical protein YOR297c - yeast (Saccharomyces cerevisiae) ; (Z75205) ORF YOR297c [Saccharomyces cerevisiae]
16737	ENU00531	ANI61C7324: 6273..5731	72-95	546-572	EST	"t2b05a1.r1, t2b05a1.fl"			43	0.002			protein-L-isoaspartate O-methyltransferase (protein-beta-aspartate methyltransferase) (PIMT) (protein L-isoaspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltransferase) ; (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]
16738	ENU00532	ANI61C1077: 4-3391..3935	42-62	522-545	EST	"o6d07a1.r1, o6d07a1.fl"			143	9E-34			titin - human
16739	ENU00533	ANI61C7767: 561..16	22-53	506-525	EST	"g3b08a1.r1, g3b08a1.fl"			35	0.46			(AJ235271) cell surface antigen (sca3) [Rickettsia prowazekii]
16740	ENU00534	ANI61C5800: 2619..3167	22-55	502-528	EST	"n0e05a1.r1, n0e05a1.fl"			32	2.3			probable ARP2/3 complex 34 KD subunit (P34-ARC) ; (Z98981)
16741	ENU00535	ANI61C598:3: 5..586	23-44	500-532	EST	"dlal1a1.r1, dlal1a1.fl"			125	2E-28			probable Arp2-3 complex subunit [Schizosaccharomyces pombe]
16742	ENU00536	ANI61C3057: 326..868	22-46	512-531	EST	"m0g08a1.r1, m0g08a1.fl"			125	2E-28			probable ARP2/3 complex 34 KD subunit (P34-ARC) ; (Z98981)
16743	ENU00537	ANI61C3057: 326..868	22-46	512-531	EST	"q0c02a1.r1, q0c02a1.fl"			125	2E-28			probable Arp2-3 complex subunit [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16744	ENU00538	ANI61C1043	69-88	559-583	EST	"p0c03a1.rl, p0c03a1.fl"							
16745	ENU00539	ANI61C319:2	24-46	513-545	EST	"w7e08a1.rl, w7e08a1.fl"							(Z50795) R166.3 [Caenorhabditis elegans]
16746	ENU00540	ANI61C8718: 21..584	42-61	530-563	EST	"n8h01a1.rl, n8h01a1.fl"							hypothetical 9.1 KD protein C23C11.12 in chromosome I;
16747	ENU00541	ANI61C7165: 1783..1218	46-65	543-569	EST	"i0d06a1.rl, i0d06a1.fl"							(Z98559) very hypothetical protein [Schizosaccharomyces pombe]
16748	ENU00542	ANI61C7165: 1783..1218	46-65	543-569	EST	"k5g04a1.rl, k5g04a1.fl"							hypothetical 9.1 KD protein C23C11.12 in chromosome I;
16749	ENU00543	ANI61C9738: 1413..1979	22-57	517-546	EST	"g6c12a1.rl, g6c12a1.fl"							(Z98559) very hypothetical protein [Schizosaccharomyces pombe]
16750	ENU00544	ANI61C9691: 444..1013	64-83	564-590	EST	"y6f09a1.rl, y6f09a1.fl"							(AF055904) unknown [Myxococcus xanthus]
16751	ENU00545	ANI61C5967: 1850..1282	46-65	547-572	EST	"c3a12a1.rl, c3a12a1.fl"							(U95843) pTP [Murine adenovirus type 1]
16752	ENU00546	ANI61C1353: 1611..2180	30-65	537-557	EST	"z4c01a1.rl, z4c01a1.fl"							(Z77135) similar to endothelin converting enzyme 1; cDNA EST yk452c2.5 comes from this gene;
16753	ENU00547	ANI61C541:2	25-56	528-553	EST	"e9f10a1.rl, e9f10a1.fl"							cDNA EST yk452c2.3 comes from this gene; cDNA EST yk357g11.3 comes from this gene; cDNA EST yk357g11.5 comes from this gene; cDNA EST ...
16754	ENU00548	ANI61C3288: 3396..2822	35-54	549-567	EST	"y8a07a1.rl, y8a07a1.fl"							(M16336) CD2 surface antigen [Homo sapiens]
16755	ENU00549	ANI61C5479: 3279..3857	44-64	545-580	EST	"w6c12a1.rl, w6c12a1.fl"							(AF035770) ribosomal protein L37 [Schistosoma mansoni]
16756	ENU00550	ANI61C8257: 1417..1996	71-91	589-608	EST	"z5g08a1.rl, z5g08a1.fl"							(U51998) C12D12.1 gene product [Caenorhabditis elegans]
16757	ENU00551	ANI61C128:2	47-65	565-585	EST	"g9b08a1.rl, g9b08a1.fl"							high-sulfur keratin - human ; (X63337) high sulfur keratin [Homo sapiens]

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16758	ENU00552	ANI61C5509: 817..235	27-46	548-567	EST	"flg08a1.r1, flg08a1.fl"			201	4E-51			"hypothetical 37.2 KD protein in CHA1-PRD1 intergenic region ; hypothetical protein YCL059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL059c, len:316 [Saccharomyces cerevisiae]"
16759	ENU00553	ANI61C597:8 01..218	72-91	594-613	EST	"n0b05a1.r1, n0b05a1.fl"			41	0.007			"hypothetical protein with neutralization-sensitive epitopes [Cryptosporidium parvum] ; (Y16243) sporozoite surface antigen p23 [Cryptosporidium parvum] surfactin synthetase component II - Bacillus subtilis (fragment) ; (D13262) surfactin synthetase [Bacillus subtilis]"
16760	ENU00554	ANI61C1027 7:2108..2694	42-61	560-586	EST	"i0f07a1.r1, i0f07a1.fl"			32	4.3			"acidic ribosomal protein P0.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (M37326) ribosomal protein L10e [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (U19028) Rpl10ep [Saccharomyces cerevisiae]"
16761	ENU00555	ANI50C392_ 2:873..394	70-89	595-615	EST	"c9e07a1.r1, c9e07a1.fl"			223	7E-58			(L25528) homologous to human cytomegalovirus UL25 gene family [Human herpesvirus 6]
16762	ENU00556	ANI61C630:2 46..833	72-94	582-617	EST	"i8c07a1.r1, i8c07a1.fl"			34	1.1			ribosomal protein S27 (metallopanstimulin 1) ; 40S ribosomal protein S27 (metallopan-stimulin 1) (MPS-1) ; growth factor-inducible zinc finger protein MPS-1 - human ; (L19739) metallopanstimulin [Homo sapiens] ; (U57847) ribosomal protein S27 [Homo sapiens]
16763	ENU00557	ANI61C3327: 119..707	59-78	585-605	EST	"m8f08a1.r1, m8f08a1.fl"			99	2E-20			putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae) ; (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
16764	ENU00558	ANI61C884:5 89..1	22-54	545-568	EST	"m8g04a1.r1, m8g04a1.fl"			98	2E-24			(AF056116) LRP1 [Fugu rubripes]
16765	ENU00559	ANI61C5819: 615..26	22-49	547-569	EST	"z3g04a1.r1, z3g04a1.fl"			31	7.5			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16766	ENU00560	ANI61C4296: 1125..535	22-49	535-570	EST	"c7e04a1.r1, c7e04a1.fl"		60	0.000000	02			(AF069523) heat shock protein Hsp88 [Neurospora crassa]
16767	ENU00561	ANI61C4371: 1085..494	24-56	553-573	EST	"l3g10a1.r1, l3g10a1.fl"		62	0.000000	004			(D85230) hypothetical protein [Plectonema boryanum]
16768	ENU00562	ANI61C9600: 36-65	36-65	568-587	EST	"q0h08a1.r1, q0h08a1.fl"		147	3E-39				hypothetical oxidoreductase in CITA-SSPB intergenic region ; (Y14082) hypothetical protein [Bacillus subtilis] ; (Z99109) similar to glucose 1-dehydrogenase [Bacillus subtilis]
16769	ENU00563	ANI61C5468: 32-52	32-52	550-583	EST	"m5d10a1.r1, m5d10a1.fl"		95	3E-19				hypothetical 49.6 KD protein in ELM1-PR12 intergenic region ; hypothetical protein YKL046c precursor - yeast (Saccharomyces cerevisiae) ; (Z28046) ORF YKL046c [Saccharomyces cerevisiae]
16770	ENU00564	ANI61C8586: 791..196	41-60	574-594	EST	"n8f01a1.r1, n8f01a1.fl"		109	2E-23				"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis] "
16771	ENU00565	ANI61C405:1 982..1384	58-77	580-613	EST	"i3b04a1.r1, i3b04a1.fl"		51	0.000006				eukaryotic translation initiation factor 1A (EIF-1A) (EIF-4C) ; translation initiation factor eIF-1A - yeast (Saccharomyces cerevisiae) ; (U11585) translation initiation factor 1A [Saccharomyces cerevisiae] ; (Z49260) Tif1p [Saccharomyces cerevisiae]
16772	ENU00566	ANI61C2419: 85..684	51-71	577-608	EST	"r4f07a1.r1, r4f07a1.fl"		160	9E-39				hypothetical 50.4 KD protein C1F8.04C in chromosome I ; (Z81312) unknown [Schizosaccharomyces pombe]
16773	ENU00567	ANI61C9395: 5609..5313	25-46	559-587	EST	"m0d12a1.r1, m0d12a1.fl"		39	0.035				(AP000001) 58aa long hypothetical protein [Pyrococcus horikoshii]
16774	ENU00568	ANI61C1253: 1..401	22-51	568-586	EST	"e9h12a1.r1, e9h12a1.fl"		46	0.0002				(AL034352) putative signal transduction protein [Schizosaccharomyces pombe]
16775	ENU00569	ANI61C1110 3:4962..4355	23-43	567-588	EST	"c6d09a1.r1, c6d09a1.fl"		34	1.2				hypothetical PXBL-I protein ; trans-activating transcriptional regulatory protein - bovine leukemia virus (fragment)
16776	ENU00570	ANI61C322:7 669..8278	46-65	585-613	EST	"w9c02a1.r1, w9c02a1.fl"		31	6				(AF079173) ORF1 protein [TT virus]
16777	ENU00571	ANI61C9395: 6467..5856	22-56	562-591	EST	"m8g07a1.r1, m8g07a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16778	ENU00572	ANI61C6494: 4383..5000	22-45	576-597	EST	"g2e12a1.r1, g2e12a1.fl"		31	31	6.1		(Y11476) hypothetical protein [Bacteriophage 12826]
16779	ENU00573	ANI61C9771: 2155..2773	29-50	571-605	EST	"o9d08a1.r1, o9d08a1.fl"		31	31	6.1		(Y13978) thrombomucin [Gallus gallus]
16780	ENU00574	ANI61C7686: 1198..578	30-50	589-608	EST	"z6h07a1.r1, z6h07a1.fl"		87	87	1E-16		(AL034583) hypothetical protein [Schizosaccharomyces pombe]
16781	ENU00575	ANI61C3783: 1110..490	24-43	583-602	EST	"w4d02a1.r1, w4d02a1.fl"		102	102	3E-21		transcription initiation factor TFIID 90 KD subunit (TAFII-90) ; TATA box-binding protein-associated factor chain TAFII90 - yeast (Saccharomyces cerevisiae) ; (Z21487) unknown [Saccharomyces cerevisiae] ; (Z36067) ORF YBR198c [Saccharomyces cerevisiae] ; TATA box-binding protein-associated factor [Saccharomyces cerevisiae]
16782	ENU00576	ANI61C9540: 114..737	22-46	567-602	EST	"g3b03a1.r1, g3b03a1.fl"		34	34	0.93		[Saccharomyces cerevisiae] (U95159) gelsolin-related protein GRP125 [Dictyostelium discoideum] (AB014462) neuronal leucine-rich repeat protein [Xenopus laevis] (Z78420) Weak similarity to Human transcription factor SP3 (SW:SP3_HUMAN); cDNA EST EMBL:C09666 comes from this gene; cDNA EST EMBL:C08071 comes from this gene [Caenorhabditis elegans]
16783	ENU00577	ANI61C8836: 2937..3563	72-92	636-655	EST	"n8h06a1.r1, n8h06a1.fl"		33	33	2.1		"(U32776) L-2,4-diaminobutyrate decarboxylase [Haemophilus influenzae Rd]" (U41994) similar to glycoproteins [Caenorhabditis elegans] (Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]
16784	ENU00578	ANI50C2177 6_1:487..1113	37-56	592-621	EST	"f0b09a1.r1, f0b09a1.fl"		35	35	0.42		hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region ; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe13p [Saccharomyces cerevisiae]
16785	ENU00579	ANI61C3301: 1648..2275	23-42	589-608	EST	"o6g06a1.r1, o6g06a1.fl"		86	86	2E-16		
16786	ENU00580	ANI61C1106 5:6001..5372	29-48	588-616	EST	"h0c06a1.r1, h0c06a1.fl"		36	36	0.24		
16787	ENU00581	ANI61C5297: 1067..435	62-81	626-651	EST	"m7h04a1.r1, m7h04a1.fl"		33	33	2.1		
16788	ENU00582	ANI61C7555: 3136..3767	22-52	576-611	EST	"y8b06a1.r1, y8b06a1.fl"		102	102	3E-38		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16789	ENU00583	ANI61C8842: 57-76	966..1597	613-646	EST	"c9e09a1.rl, c9e09a1.fl"		34	0.72			(Z92782) F14F8.4 [Caenorhabditis elegans]
16790	ENU00584	ANI61C8836: 72-94	2929..3563	644-663	EST	"w4c01a1.rl, w4c01a1.fl"		33	2.1			(AB014462) neuronal leucine-rich repeat protein [Xenopus laevis]
16791	ENU00585	ANI61C3242: 41-60	307..949	621-641	EST	"x9c11a1.rl, x9c11a1.fl"		123	1E-27			hypothetical 31.5 KD protein ; (U05664) homologous to Swiss-Prot Accession Number P20435: Saccharomyces cerevisiae RNA polymerase subunit RPO26 [Sulfolobus acidocaldarius]
16792	ENU00586	ANI61C7237: 22-46	2093..1450	604-623	EST	"x5h08a1.rl, x5h08a1.fl"		32	4.9			"Allergen ARA H 1, clone P17 (ARA H1) ; (L38853) Ara h 1 [Arachis hypogaea]"
16793	ENU00587	ANI61C1080: 36-62	1883..2530	620-641	EST	"z4f12a1.rl, z4f12a1.fl"		222	2E-57			(AF051914) C-4 methyl sterol oxidase [Candida albicans]
16794	ENU00588	ANI61C353:3 22-47	055..3702	594-627	EST	"a0g03a1.rl, a0g03a1.fl"		31	6.5			hypothetical 46.4 KD protein SLL1917 ; (D90904) oxygen independent coprophorinogen III oxidase [Synechocystis sp.]
16795	ENU00589	ANI61C7994: 52-78	5677..5028	637-659	EST	"t2a09a1.rl, t2a09a1.fl"		123	8E-28			(AL033391) hypothetical membrane protein [Candida albicans]
16796	ENU00590	ANI61C8252: 22-42	2731..2079	597-632	EST	"r2h04a1.rl, r2h04a1.fl"		78	1E-18			F-actin capping protein alpha subunit ; actin-capping protein alpha chain - yeast (Saccharomyces cerevisiae) ; (X61398) Capping Protein Alpha Subunit [Saccharomyces cerevisiae] ; (Z28007) ORF YKL007w [Saccharomyces cerevisiae] ; (S59773) CAP1 [Saccharomyces cerevisiae]
16797	ENU00591	ANI61C2704: 62-85	358..1011	638-673	EST	"h1d05a1.rl, h1d05a1.fl"		37	0.15			Exocyst complex component SEC3 (PSL1 protein) ; PSL1 protein - yeast (Saccharomyces cerevisiae) ; (L22204) Psl1p [Saccharomyces cerevisiae] ; (U18778) Sec3p [Saccharomyces cerevisiae]
16798	ENU00592	ANI61C14:16 24-47	46..2300	608-636	EST	"t2d08a1.rl, t2d08a1.fl"		32	5			probable phosphatidylserine synthase PEL1 - yeast (Saccharomyces cerevisiae)
16799	ENU00593	ANI61C4315: 62-94	4444..3788	655-676	EST	"o9f07a1.rl, o9f07a1.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16800	ENU00594	ANI61C3288: 35-54 3396..2737	22-51	612-640	EST	"y6h10a1.rl, y6h10a1.fl"		63	32	5.1			(AF035770) ribosomal protein L37 [Schistosoma mansoni] (U47849) Lozenge [Drosophila melanogaster]
16801	ENU00595	ANI61C1113 1:258..918	22-51	615-641	EST	"r4b11a1.rl, r4b11a1.fl"		33	33	1.7			hypothetical 118.4 KD protein in BAT2-DAL5 intergenic region precursor ; probable membrane protein
16802	ENU00596	ANI61C3266: 22-53 3466..2805	22-53	615-641	EST	"a0h04a1.rl, a0h04a1.fl"							YJR151c - yeast (Saccharomyces cerevisiae) ; (Z49651) ORF YJR151c [Saccharomyces cerevisiae]
16803	ENU00597	ANI61C9578: 61-80 6806..6144	61-80	647-681	EST	"w6g09a1.rl, w6g09a1.fl"		40	35	0.018			(AL031031) hypothetical protein SC7C7.09 [Streptomyces coelicolor] (Z78420) Weak similarity to Human transcription factor SP3 (SW:SP3_HUMAN); cDNA EST EMBL:C09666 comes from this gene; cDNA EST EMBL:C08071 comes from this gene [Caenorhabditis elegans]
16804	ENU00598	ANI50C2177 6_1:451..1114	27-52	626-648	EST	"z3d05a1.rl, z3d05a1.fl"							(L26122) matrix protein [Mumps virus]
16805	ENU00599	ANI61C7657: 70-89 871..1535	70-89	662-692	EST	"d4b01a1.rl, d4b01a1.fl"		34	61	1			hypothetical 13.9 KD protein C2E11.03C in chromosome I ; (AL031181) very hypothetical protein [Schizosaccharomyces pombe] ; (AL035064) very hypothetical protein [Schizosaccharomyces pombe]
16806	ENU00600	ANI61C187:9 75..310	22-46	621-645	EST	"q0h12a1.rl, q0h12a1.fl"							hypothetical 23.7 KD protein in NMD5-HOM6 intergenic region ; hypothetical protein YJR133w - yeast (Saccharomyces cerevisiae) ; (Z49633) ORF YJR133w [Saccharomyces cerevisiae]
16807	ENU00601	ANI61C5803: 22-56 2406..1760	22-56	611-646	EST	"d5f05a1.rl, d5f05a1.fl"							(Z47973) ORF L0596 [Saccharomyces cerevisiae]
16808	ENU00602	ANI61C6798: 31-50 5067..5734	31-50	633-656	EST	"b0g07a1.rl, b0g07a1.fl"		46	53	0.0002			histone H2B ; histone H2B - Emericella nidulans ; (X55547) H2B [Emericella nidulans] ; histone H2B [Emericella nidulans]
16809	ENU00603	ANI61C1042 6:1247..579	22-50	629-648	EST	"r7c08a1.rl, r7c08a1.fl"							
16810	ENU00604	ANI61C7674: 26-46 1339..2007	26-46	626-652	EST	"g4c06a1.rl, g4c06a1.fl"			62	2E-34			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16811	ENU00605	ANI61C1080: 1861..2530	22-49	628-649	EST	"g4f03a1.r1, g4f03a1.fl"		32	5.1				"Allergen ARA H 1, clone P17 (ARA H 1); (L38853) Ara h 1 [Arachis hypogaea]"
16812	ENU00606	ANI61C1100: 4016..3347	22-49	625-649	EST	"l3e08a1.r1, l3e08a1.fl"		37	0.001				hypothetical 15.7 KD protein in UBP1-HNT1 intergenic region; probable membrane protein YDL123w - yeast (Saccharomyces cerevisiae); (Z74171) ORF YDL123w [Saccharomyces cerevisiae]
16813	ENU00607	ANI61C2308: 79..749	22-53	631-650	EST	"g5g06a1.r1, g5g06a1.fl"		45	0.0004				Conidiation-specific protein 8; con-8 protein - Neurospora crassa; (X07040) con-8 [Neurospora crassa]
16814	ENU00608	ANI61C3183: 491..1165	37-56	637-669	EST	"w8f02a1.r1, w8f02a1.fl"		33	0.001				NADH-ubiquinone oxidoreductase B22 subunit (complex I-B22) (CI-B22); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine; (X64836) NADH-ubiquinone oxidoreductase complex B22 subunit [Bos taurus]
16815	ENU00609	ANI61C9395: 6555..5879	69-88	670-703	EST	"o8b09a1.r1, o8b09a1.fl"		31	6.9				(AF079173) ORF1 protein [TT virus]
16816	ENU00610	ANI61C1077: 4-2433..1757	22-45	630-656	EST	"c6a04a1.r1, c6a04a1.fl"		33	2.3				(U89341) phosphoglucomutase 1 [Zea mays]
16817	ENU00611	ANI61C2136: 4474..3796	22-44	635-658	EST	"g3a02a1.r1, g3a02a1.fl"		48	0.00005				Long-chain-fatty-acid--CoA ligase 4 (long-chain acyl-CoA synthetase 4) (fatty acid activator 4); long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) FAA4 - yeast (Saccharomyces cerevisiae); (Z48756) unknown [Saccharomyces cerevisiae]
16818	ENU00612	ANI61C3715: 10..689	31-54	638-667	EST	"j9f11a1.r1, j9f11a1.fl"		62	0.000000	003			hypothetical 17.5 KD protein in chromosome II; (AL022103) hypothetical protein [Schizosaccharomyces pombe]
16819	ENU00613	ANI61C9064: 375..1062	50-69	660-695	EST	"l3d12a1.r1, l3d12a1.fl"		34	1.1				(U96771) unknown [Prevotella bryantii]
16820	ENU00614	ANI61C8444: 1586..2274	56-74	682-702	EST	"j0c06a1.r1, j0c06a1.fl"		136	1E-31				(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16821	ENU00615	ANI61C7805: 4521..5220	36-56	666-693	EST	"g4c12a1.r1, g4c12a1.fl"			40	0.019			hypothetical 8.2 KD protein C26A3.14C in chromosome I ; (Z69240) very hypothetical protein [Schizosaccharomyces pombe]
16822	ENU00616	ANI61C884:7 03..1	26-46	663-686	EST	"g6c01a1.r1, g6c01a1.fl"			98	4E-27			putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae) ; (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
16823	ENU00617	ANI61C9578: 6806..6103	42-61	678-703	EST	"k0d01a1.r1, k0d01a1.fl"			40	0.019			(AL031031) hypothetical protein SC7C7.09 [Streptomyces coelicolor]
16824	ENU00618	ANI61C9152: 1281..1985	27-47	670-689	EST	"m8f07a1.r1, m8f07a1.fl"			85	4E-16			(AL049559) hypothetical protein [Schizosaccharomyces pombe]
16825	ENU00619	ANI61C8549: 2986..3690	22-52	657-684	EST	"w6e07a1.r1, w6e07a1.fl"			34	1.4			hypothetical 15.6 KD protein in CSN-ADHB intergenic region ; (U93875) Yra1 [Bacillus subtilis] ; (X92868) unknown [Bacillus subtilis] ; (Z99117) similar to hypothetical proteins from B. subtilis [Bacillus subtilis]
16826	ENU00620	ANI61C9745: 4683..3978	42-63	687-705	EST	"s9f03a1.r1, s9f03a1.fl"			46	0.000000			small nuclear ribonucleoprotein SM D2 (SNRNP core protein D2) (SM-D2) ; small nuclear ribonucleoprotein chain D2 - human ; (U15008) Sm D2 [Homo sapiens] ; (AC007191) SMD2_HUMAN; SNRNP core protein D2; SM-D2 [Homo sapiens]
16827	ENU00621	ANI61C9745: 4683..3978	42-63	687-705	EST	"w9g09a1.r1, w9g09a1.fl"			46	0.000000			small nuclear ribonucleoprotein SM D2 (SNRNP core protein D2) (SM-D2) ; small nuclear ribonucleoprotein chain D2 - human ; (U15008) Sm D2 [Homo sapiens] ; (AC007191) SMD2_HUMAN; SNRNP core protein D2; SM-D2 [Homo sapiens]
16828	ENU00622	ANI50C6889 _1:1625..916	50-69	686-717	EST	"dlf10a1.r1, dlf10a1.fl"			199	2E-50			probable membrane protein YPL134c - yeast (Saccharomyces cerevisiae) ; (U43703) Lpi1 Ip [Saccharomyces cerevisiae]
16829	ENU00623	ANI61C7675: 5310..4598	43-75	682-713	EST	"o0c10a1.r1, o0c10a1.fl"			32	5.6			(AB001347) brain beta 3 spectrin [Rattus norvegicus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16830	ENU00624	ANI61C1679; 2377..1661	34-57	678-707	EST	"o0e10a1.r1, o0e10a1.fl"			32	4.3			(X03541) trk gene product (aa 1-641) [Homo sapiens] ; gene oncD [Homo sapiens]
16831	ENU00625	ANI61C7987; 29-48	29-48	683-702	EST	"t2e02a1.r1, t2e02a1.fl"			72	4E-12			(AL035655) 60s ribosomal protein l36 [Schizosaccharomyces pombe]
16832	ENU00626	ANI61C1126; 282..997	28-48	679-701	EST	"i0d04a1.r1, i0d04a1.fl"			92	2E-33			40S ribosomal protein S17 ; (M13933) ribosomal protein S17 [Cricetulus griseus] ; (D25213) ribosomal protein S17 [Mus musculus]
16833	ENU00627	ANI61C6923; 1761..1045	22-45	672-696	EST	"d5g10a1.r1, d5g10a1.fl"			35	0.5			(AF014795) cytochrome P450 30 [Mercenaria mercenaria]
16834	ENU00628	ANI61C9637; 4095..4814	46-68	704-723	EST	"h0d10a1.r1, h0d10a1.fl"			214	1E-55			Peptidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
16835	ENU00629	ANI61C9637; 4095..4814	35-57	693-712	EST	"g6g11a1.r1, g6g11a1.fl"			214	1E-55			Peptidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
16836	ENU00630	ANI61C9637; 4095..4814	40-62	698-717	EST	"o6a07a1.r1, o6a07a1.fl"			214	1E-55			Peptidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16837	ENU00631	ANI61C7067: 24-49 869..148		674-703	EST	"i7f01a1.r1, i7f01a1.fl"			178	4E-44			Mannitol-1-phosphate 5-dehydrogenase ; mannitol-1-phosphate dehydrogenase - Bacillus subtilis (fragment) ; (D38161) mannitol-1-phosphate dehydrogenase [Bacillus subtilis] ; (D50453) homologue of mannitol-1- phosphate dehydrogenase of Streptococcus mutans [Bacillus subtilis] ; (Z99106) mannitol-1- phosphate dehydrogenase [Bacillus subtilis] ; mannitol-1-phosphate dehydrogenase [Bacillus subtilis] (AL033391) conserved hypothetical protein [Candida albicans] GAG polypeptide [contains: inner coat protein P12; core protein P15; core shell protein P30; nucleoprotein P10] ; gag polypeptide - baboon endogenous virus (strain M7) ; (X05470) gag gene product (AA 1-537) [Baboon endogenous virus] ; (D10032) polypeptide [Baboon endogenous virus] ; (M16550) gag polypeptide [Baboon endogenous virus]
16838	ENU00632	ANI61C1010 32-53 1:5322..4598		682-714	EST	"t2a12a1.r1, t2a12a1.fl"			87	6E-23			
16839	ENU00633	ANI61C6349: 51-70 940..130		714-734	EST	"k5d10a1.r1, k5d10a1.fl"			34	1.5			
16840	ENU00634	ANI61C3091: 33-52 559..1284		681-716	EST	"y3d09a1.r1, y3d09a1.fl"			42	0.000000			
16841	ENU00635	ANI61C6349: 56-75 940..130		719-739	EST	"i2e02a1.r1, i2e02a1.fl"			34	1.5			GAG polypeptide [contains: inner coat protein P12; core protein P15; core shell protein P30; nucleoprotein P10] ; gag polypeptide - baboon endogenous virus (strain M7) ; (X05470) gag gene product (AA 1-537) [Baboon endogenous virus] ; (D10032) polypeptide [Baboon endogenous virus] ; (M16550) gag polypeptide [Baboon endogenous virus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16842	ENU00636	ANI61C1031 8:1119..849	52-75	716-737	EST	"y6a08a1.r1, y6a08a1.fl"		92	3E-18				"probable 60S ribosomal protein YIL052C ; ribosomal protein L34.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77, RL34_RAT P11250 60S ribosomal protein L34 [Saccharomyces cerevisiae]"
16843	ENU00637	ANI61C7768: 51..778	62-81	716-747	EST	"m0g07a1.r1, m0g07a1.fl"		142	5E-55				(AL023518) Tal1p transaldolase [Schizosaccharomyces pombe]
16844	ENU00638	ANI61C6509: 1025..295	70-90	737-758	EST	"a0f04a1.r1, a0f04a1.fl"		33	2				(U34781) Antho-LWamidII preprohormone [Anthopleura elegantissima] ; prepro-hormone [Anthopleura elegantissima]
16845	ENU00639	ANI61C3368: 7507..8240	44-63	709-735	EST	"y8d01a1.r1, y8d01a1.fl"		262	6E-75				aminopeptidase Y (EC 3.4.11.-) precursor - yeast (Saccharomyces cerevisiae)
16846	ENU00640	ANI61C1096 0:2340..3077	70-89	746-764	EST	"k0h03a1.r1, k0h03a1.fl"		37	0.17				(M94288) Nopp140 [Rattus norvegicus]
16847	ENU00641	ANI61C1537: 1654..917	48-68	711-742	EST	"g9f06a1.r1, g9f06a1.fl"		86	3E-16				(U16137) Mvp1p [Saccharomyces cerevisiae]
16848	ENU00642	ANI61C2890: 6590..5853	50-69	717-745	EST	"r5g07a1.r1, r5g07a1.fl"		32	4.5				"(D90129) T-cell receptor beta chain, leader sequence, variable region, diversity region and joining region [Bos taurus]"
16849	ENU00643	ANI61C9959: 1129..1867	41-62	704-737	EST	"d5h12a1.r1, d5h12a1.fl"		34	1.5				hypothetical 36.9k protein - Acetobacter pasteurianus plasmid AP12875 ; (U20550) protein A [Acetobacter pasteurianus]
16850	ENU00644	ANI61C9172: 1232..1971	30-49	706-727	EST	"m5d05a1.r1, m5d05a1.fl"		35	0.68				(Z67882) similar to p-glycoprotein (MDR) [Caenorhabditis elegans]
16851	ENU00645	ANI61C8729: 1741..2481	57-75	723-755	EST	"y8h03a1.r1, y8h03a1.fl"		34	0.89				(AF100656) contains weak similarity to Plasmodium yoelii rhopty protein S6 (GB:U36927) [Caenorhabditis elegans]
16852	ENU00646	ANIC9281_1: 750..1	53-72	730-760	EST	"y8e11a1.r1, y8e11a1.fl"		441	e-123				(AF053883) coatomer alpha subunit [Emericella nidulans]
16853	ENU00647	ANI61C1053 9:976..226	26-50	706-734	EST	"r4b09a1.r1, r4b09a1.fl"							
16854	ENU00648	ANI61C9111: 5741..6491	29-51	718-737	EST	"c5b03a1.r1, c5b03a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16855	ENU00649	ANI61C1048 3:4098..4851	22-43	714-733	EST	"g9e11a1.r1, g9e11a1.fl"			48	0.00005			(AL023534) hypothetical protein [Schizosaccharomyces pombe]
16856	ENU00650	ANI61C4054; 248..1007	22-51	708-739	EST	"c9d08a1.r1, c9d08a1.fl"			43	0.003			factor 3 [Thermomyces lanuginosus] (AF042103) tat protein [Human immunodeficiency virus type 1]
16857	ENU00651	ANI61C1080 1:769..6	22-52	723-743	EST	"n8f04a1.r1, n8f04a1.fl"			33	2.1			putative mitochondrial carrier YER053C ; hypothetical protein YER053c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer053cp [Saccharomyces cerevisiae]
16858	ENU00652	ANI61C1027 7:7366..6602	31-51	718-753	EST	"j9a02a1.r1, j9a02a1.fl"			159	2E-38			
16859	ENU00653	ANI61C8646; 2416..1650	34-54	729-758	EST	"g3c08a1.r1, g3c08a1.fl"			56	0.000000 2			"(U48363) alpha-NAC, muscle-specific form gp220 [Mus musculus] ; (U48364) alpha-NAC, muscle-specific form gp220 [Mus musculus] "
16860	ENU00654	ANI61C2324; 1280..514	65-87	766-790	EST	"r5c11a1.r1, r5c11a1.fl"			118	4E-26			crml+ protein - fission yeast (Schizosaccharomyces pombe)
16861	ENU00655	ANI61C3531; 1196..418	55-82	760-791	EST	"a0c01a1.r1, a0c01a1.fl"			32	3.6			"phosphatidylinositol 3-kinase catalytic subunit, delta isoform (PI3-kinase P110 subunit delta) (PTDINS-3-kinase P110) (PI3K) (P110delta) ; (U86587) phosphatidylinositol 3-kinase catalytic subunit p110 delta [Mus musculus] "
16862	ENU00656	ANI61C7922; 4398..3619	22-42	738-759	EST	"p0g04a1.r1, p0g04a1.fl"			46	0.0003			"mitochondrial 60S ribosomal protein MRP49 precursor ; ribosomal protein MRP49, mitochondrial - yeast (Saccharomyces cerevisiae) ; (M81697) mitochondrial ribosomal protein [Saccharomyces cerevisiae] ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28167) ORF YKL167c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] "
16863	ENU00657	ANI61C8803; 2388..1609	30-50	741-767	EST	"w9h07a1.r1, w9h07a1.fl"			35	0.72			(Z81523) Similarity to Bovine protooncogene C-MYB (TR:Q28080); cDNA EST EMBL:D32371 comes from this gene; cDNA EST EMBL:D34735 comes from this gene; cDNA EST EMBL:D37111 comes from this gene; cDNA EST EMBL:D71956 comes from thi...

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16864	ENU00658	ANI61C4078: 1227..448	57-77	767-794	EST	"o0a12a1.rl, o0a12a1.fl"		34	34	1.6			(M13790) albumin 1 [Pisum sativum]
16865	ENU00659	ANI61C6432: 1618..833	43-76	751-786	EST	"c6c05a1.rl, c6c05a1.fl"		36	36	0.25			hypothetical 18.9 KD protein in GCN20-CMK1 intergenic region ; hypothetical protein YFR011c - yeast (Saccharomyces cerevisiae) ; (D50617) YFR011C [Saccharomyces cerevisiae] ; (D44599) ochre suppressor tyr-tRNA (sup4) [Saccharomyces cerevisiae] (U29096) coded for by C. elegans cDNA CEESU96F; coded for by C. elegans cDNA CEESU96F; similar to C. elegans proteins ZC84.1 and ZC84.6 ; also similar to serine protease inhibitors (members of BPTI/Kunitz family of inhibitors) [Caenorhabditis... "N,O-diacetylmuramidase (lysozyme CH) ; lysozyme (EC 3.2.1.17) - fungus (Chalara sp.)"
16866	ENU00660	ANI61C685:4 45-67 4..832	45-67	764-791	EST	"j9g05a1.rl, j9g05a1.fl"		32	32	4.8			hypothetical 8.2 KD protein C26A3.14C in chromosome I ; (Z69240) very hypothetical protein [Schizosaccharomyces pombe] (AF093540) ribosomal protein L26 [Zea mays]
16868	ENU00662	ANI61C757:1 532..2322	56-75	780-804	EST	"g2c04a1.rl, g2c04a1.fl"		40	40	0.022			endoplasmic reticulum membrane protein SHR3 - yeast (Saccharomyces cerevisiae) ; (X99000) secretory component [Saccharomyces cerevisiae] ; (Z74260) ORF YDL212w [Saccharomyces cerevisiae]
16869	ENU00663	ANI61C7805: 4476..5266	58-77	786-806	EST	"z1d03a1.rl, z1d03a1.fl"		115	69	3E-25			thioredoxin H-type 2 (TRX-H2) ; thioredoxin h2 - common tobacco ; (Z11803) thioredoxin [Nicotiana tabacum] ; thioredoxin [Nicotiana tabacum]
16870	ENU00664	ANI61C1473: 3701..4495	55-76	781-807	EST	"h4a07a1.rl, h4a07a1.fl"		34	34	1.7			thioredoxin [Nicotiana tabacum]
16871	ENU00665	ANI50C2006 8_1:1456..2253	22-44	757-777	EST	"j0c07a1.rl, j0c07a1.fl"		31	31	8.4			thioredoxin [Nicotiana tabacum]
16872	ENU00666	ANI61C8263: 1773..976	25-44	761-781	EST	"r4a09a1.rl, r4a09a1.fl"		31	31	8.4			thioredoxin [Nicotiana tabacum]
16873	ENU00667	ANI61C5890: 298..1097	71-90	802-828	EST	"e0a12a1.rl, e0a12a1.fl"		31	31	8.4			thioredoxin [Nicotiana tabacum]

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16874	ENU00668	ANI61C9181: 2043..2843	35-58	768-793	EST	"y8e04a1.rl, y8e04a1.fl"		38	0.11			[X95677] argBPIB [Homo sapiens]
16875	ENU00669	ANI61C5479: 3056..3857	22-51	746-781	EST	"o6f11a1.rl, o6f11a1.fl"		36	0.33			[U51998] C12D12.1 gene product [Caenorhabditis elegans]
16876	ENU00670	ANI61C5479: 3056..3857	22-51	746-781	EST	"m6c01a1.rl, m6c01a1.fl"		36	0.33			[U51998] C12D12.1 gene product [Caenorhabditis elegans]
16877	ENU00671	ANI61C5479: 3052..3857	22-51	750-785	EST	"g9b05a1.rl, g9b05a1.fl"		36	0.33			[U51998] C12D12.1 gene product [Caenorhabditis elegans]
16878	ENU00672	ANI61C5479: 3050..3857	22-50	752-787	EST	"c7f06a1.rl, c7f06a1.fl"		36	0.33			[U51998] C12D12.1 gene product [Caenorhabditis elegans]
16879	ENU00673	ANI61C6923: 1896..1088	53-72	785-819	EST	"g8g01a1.rl, g8g01a1.fl"		35	0.57			[AF014795] cytochrome P450 30 [Mercenaria mercenaria]
16880	ENU00674	ANI61C8986: 4553..3743	69-88	803-836	EST	"c9b09a1.rl, c9b09a1.fl"		131	6E-30			[AL031798] 40s ribosomal protein s20. [Schizosaccharomyces pombe]
16881	ENU00675	ANI61C8585: 4159..3348	27-47	777-796	EST	"z2h10a1.rl, z2h10a1.fl"		35	0.76			Double-strand-break repair protein RAD21 ; rad21 protein - fission yeast (Schizosaccharomyces pombe) ; (M96437) putative [Schizosaccharomyces pombe] ; [AL023781] double-strand-break repair protein Rad21p [Schizosaccharomyces pombe]
16882	ENU00676	ANI61C5319: 134..949	50-70	803-823	EST	"m8c02a1.rl, m8c02a1.fl"		32	3.8			(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia burgdorferi]
16883	ENU00677	ANI61C3974: 2143..1324	22-53	773-799	EST	"j9d07a1.rl, j9d07a1.fl"		62	3E-16			hypothetical 11.8 KD protein C1B3.02C in chromosome I ; (Z98598) hypothetical protein [Schizosaccharomyces pombe]
16884	ENU00678	ANI61C6288: 2371..3191	46-68	794-824	EST	"m6g04a1.rl, m6g04a1.fl"		62	6E-18			(U81827) 8 kDa cytoplasmic dynein light chain [Emmericella nidulans]
16885	ENU00679	ANI61C4570: 1255..2076	24-43	768-803	EST	"l0a12a1.rl, l0a12a1.fl"		99	3E-20			GTP-binding protein ypt5 - fission yeast (Schizosaccharomyces pombe)
16886	ENU00680	ANI61C8349: 495..1322	28-50	789-813	EST	"b0h11a1.rl, b0h11a1.fl"		135	2E-37			"(AL031856) atp synthase gamma chain, mitochondrial precursor [Schizosaccharomyces pombe] "
16887	ENU00681	ANI61C9418: 845..14	28-52	782-817	EST	"o6f03a1.rl, o6f03a1.fl"		55	0.000000	5		(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16888	ENU00682	ANI61C6226: 10431..9594	22-49	794-818	EST	"j0c01a1.r1, j0c01a1.fl"		53	0.000003				hypothetical 31.5 KD protein C15A10.09C in chromosome I; (Z97208) hypothetical protein [Schizosaccharomyces pombe] (Z81460) cDNA EST EMBL:D73695 comes from this gene; cDNA EST EMBL:D71097 comes from this gene; cDNA EST yk274d11.3 comes from this gene; cDNA EST yk274d11.5 comes from this gene [Caenorhabditis elegans]
16889	ENU00683	ANI61C878.3 54-76 931..3092	54-76	828-851	EST	"q0d08a1.r1, q0d08a1.fl"		40	0.024				hypothetical 90.8 KD protein T05H10.7 in chromosome II; (Z47811) similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL:D27842 comes from this gene; cDNA EST EMBL:D27841 comes from this gene; cDNA EST EMBL:D32990 comes from this gene; cDNA EST EMBL:D35712 comes...; (Z47812) similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL:D27842 comes from this gene; cDNA EST EMBL:D27841 comes from this gene; cDNA EST EMBL:D32990 comes from this gene; cDNA EST EMBL:D35712 comes...
16891	ENU00685	ANI61C1144 41-61 2:601..1451	41-61	819-849	EST	"l3h06a1.r1, l3h06a1.fl"		38	0.071				S59/4 homeotic protein - fruit fly (Drosophila melanogaster)
16892	ENU00686	ANI61C9218: 36-55 2868..2007	36-55	825-855	EST	"z1g12a1.r1, z1g12a1.fl"		218	4E-56				Lipoamide acyltransferase component precursor of branched-chain alpha-keto acid dehydrogenase complex (E2) (dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit); dihydrolipoamide transacylase precursor - mouse; (L42996) acyltransferase [Mus musculus]; branched chain alpha-ketoacid dehydrogenase:subunit=E2 [Mus musculus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16893	ENU00687	ANI61C8190: 107..972	34-62	823-857	EST	"i0a12a1.r1, i0a12a1.fl"			50	0.00002			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16894	ENU00688	ANI61C8179: 28-56 768..1633	28-56	828-851	EST	"i3g02a1.r1, i3g02a1.fl"			32	7.1			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16895	ENU00689	ANI61S262:1 22-48 55..9	22-48	822-846	EST	"r7d07a1.r1, r7d07a1.fl"			337	e-105			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16896	ENU00690	ANI61C8190: 34-62 107..977	34-62	827-862	EST	"r2f06a1.r1, r2f06a1.fl"			50	0.00002			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16897	ENU00691	ANI61C353:2 27-56 718..3588	27-56	832-855	EST	"i0b10a1.r1, i0b10a1.fl"			307	9E-83			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16898	ENU00692	ANI61C7950: 44-64 4700..3828	44-64	840-873	EST	"c1d09a1.r1, c1d09a1.fl"			34	0.28			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16899	ENU00693	ANI61C7751: 69-89 48..919	69-89	877-898	EST	"x7e04a1.r1, x7e04a1.fl"			34	1.4			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16900	ENU00694	ANI61C1473: 27-46 3649..4525	27-46	830-861	EST	"t2b06a1.r1, t2b06a1.fl"			115	3E-25			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16901	ENU00695	ANI61C560:8 22-49 1..959	22-49	838-857	EST	"h4e06a1.r1, h4e06a1.fl"			35	0.83			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16902	ENU00696	ANI61C8403: 27-56 687..1574	27-56	842-872	EST	"k5c08a1.r1, k5c08a1.fl"			188	4E-47			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16903	ENU00697	ANI61C6874: 22-48 1796..935	22-48	847-867	EST	"c9c06a1.r1, c9c06a1.fl"			185	7E-69			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)
16904	ENU00698	ANI61C4183: 23-42 2..893	23-42	837-872	EST	"o8c11a1.r1, o8c11a1.fl"			35	0.85			Thaumatin-like pathogenesis-related protein 1 precursor ; (L39774)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16905	ENU00699	ANI61C1112 8:1455..560	22-53	844-875	EST	"j9c05a1.r1, j9c05a1.fl"			37	0.22			(Z83317) cDNA EST EMBL:D36535 comes from this gene [Caenorhabditis elegans]
16906	ENU00700	ANI61C1095: 1317..418	38-58	865-895	EST	"p0c12a1.r1, p0c12a1.fl"		91	4E-19				hypothetical 16.2 KD protein C4F8.01 in chromosome I; (Z98530) hypothetical protein [Schizosaccharomyces pombe]
16907	ENU00701	ANI61C6422: 116..1018	60-79	900-920	EST	"m8h02a1.r1, m8h02a1.fl"		116	2E-25				hypothetical 62.8 KD protein in SSE1-CAR1 intergenic region; probable membrane protein YPL109c - yeast (Saccharomyces cerevisiae); (U43503) Lph17p [Saccharomyces cerevisiae] (AB002371) KIAA0373 [Homo sapiens] ubiquitin-like protein 9 - Arabidopsis thaliana (M69057) GABA-alpha receptor [Drosophila melanogaster]
16908	ENU00702	ANI61C1113 9:150..1055	34-53	879-897	EST	"j7d09a1.r1, j7d09a1.fl"		36	0.29				TOXD protein; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
16909	ENU00703	ANI61C3229: 1018..1925	22-49	856-887	EST	"s9c03a1.r1, s9c03a1.fl"		117	5E-28				
16910	ENU00704	ANI61C1209: 14407..13498	41-60	889-908	EST	"x8e02a1.r1, x8e02a1.fl"		34	1.1				
16911	ENU00705	ANI61C6421: 11040..10129	50-71	900-919	EST	"d5c07a1.r1, d5c07a1.fl"		85	9E-16				
16912	ENU00706	ANI61C878:2 079..1168	22-56	860-891	EST	"j0d05a1.r1, j0d05a1.fl"		96	1E-27				(AB017593) MBF1 [Saccharomyces cerevisiae]
16913	ENU00707	ANI61C4912: 2045..2962	48-83	895-923	EST	"j7h09a1.r1, j7h09a1.fl"		34	1.5				(D31765) KIAA0061 [Homo sapiens]
16914	ENU00708	ANI61C9205: 1105..2025	59-79	910-937	EST	"e9g09a1.r1, e9g09a1.fl"		326	1E-88				heat shock protein HSP1 (65 KD IGE-binding protein); (U92465) heat shock protein [Aspergillus fumigatus]
16915	ENU00709	ANI61C5619: 1134..986	39-62	896-926	EST	"k5b07a1.r1, k5b07a1.fl"		69	4E-11				probable transcription factor YPL230w - yeast (Saccharomyces cerevisiae); (X94561) transcription factor [Saccharomyces cerevisiae]; (Z73586) ORF YPL230w [Saccharomyces cerevisiae]
16916	ENU00710	ANI61C4416: 1283..2213	63-82	918-951	EST	"o9c12a1.r1, o9c12a1.fl"		40	0.027				110 KD antigen (PK110); 110k antigen - Plasmodium knowlesi (fragment); (M19152) 110k dalton antigen [Plasmodium knowlesi]
16917	ENU00711	ANI61C1027 9:8355..9296	22-49	890-921	EST	"z5f08a1.r1, z5f08a1.fl"							

Seq num	Seq id	Primer	Primer	Selection	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16918	ENU00712	Contig Source 5 pos 22-48	3 pos 897-922	EST	"w9c03a1.r1, w9c03a1.fl"		92	108	3E-27			(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
16919	ENU00713	ANI61C8351: 4794..5737 ANI61C5444: 32-51 1810..867	914-933	EST	"g4d03a1.r1, g4d03a1.fl"				6E-23			(AL034489) predicted using Genefinder; cDNA EST yk367h5.3 comes from this gene; cDNA EST yk367h5.5 comes from this gene; cDNA EST EMBL:Z14572 comes from this gene [Caenorhabditis elegans]
16920	ENU00714	ANI61C1141 45-64 1:1207..269	929-948	EST	"m0f05a1.r1, m0f05a1.fl"		187		1E-46			(D49367) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]
16921	ENU00715	ANI61C1057 22-55 7:1157..269	908-925	EST	"o0e11a1.r1, o0e11a1.fl"		35		0.69			hypothetical 29.3 KD protein C3F10.08C in chromosome I; (Z69369) hypothetical protein [Schizosaccharomyces pombe]
16922	ENU00716	ANI61C9395: 24-43 6836..5890	895-928	EST	"d4c02a1.r1, d4c02a1.fl"		36		0.31			hypothetical protein (sdsB region) - Pseudomonas sp
16923	ENU00717	ANI61C8649: 69-88 4267..5218	953-978	EST	"y6c07a1.r1, y6c07a1.fl"		42		0.005			(AL031013) putative secreted protein [Streptomyces coelicolor]
16924	ENU00718	ANI61C4368: 22-44 202..1159	915-937	EST	"d5a01a1.r1, d5a01a1.fl"		34		1.6			kinetoplast-associated protein - Trypanosoma cruzi; (M25364) kinetoplast-associated protein [Trypanosoma cruzi]
16925	ENU00719	ANI61C3644: 26-50 842..4594	919-947	EST	"l3f05a1.r1, l3f05a1.fl"		33		2.7			Purine nucleoside phosphorylase (inosine phosphorylase) (PNP); purine-nucleoside phosphorylase (EC 2.4.2.1) - Escherichia coli; (M60917) purine nucleoside phosphorylase [Escherichia coli]; (U14003) purine-nucleoside phosphorylase [Escherichia coli]; (AE000508) purine-nucleoside phosphorylase [Escherichia coli] GTP-binding protein ypt5 - fission yeast (Schizosaccharomyces pombe)
16926	ENU00720	ANI61C4570: 33-56 1063..2039	931-966	EST	"l3g11a1.r1, l3g11a1.fl"		132		1E-37			hypothetical 37.7 KD protein C18B11.06 in chromosome I; hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe); (Z50728) hypothetical protein [Schizosaccharomyces pombe]
16927	ENU00721	ANI61C8257: 40-59 19..1006	964-985	EST	"o6e02a1.r1, o6e02a1.fl"		85		9E-16			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16928	ENU00722	ANI61C9555: 4133..5128	72-94	1004-1023	EST	"q0a07a1.rl, q0a07a1.fl"			34	1.7			interleukin 4 receptor precursor; CD124; interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen); (X52425) interleukin 4 receptor [Homo sapiens]; (AC004525) Interleukin 4 alpha-chain precursor [Homo sapiens]
16929	ENU00723	ANI61C2666: 22-55 5004..4007	22-55	943-976	EST	"y7b01a1.rl, y7b01a1.fl"		199		2E-50			Pyrroline-5-carboxylate reductase (P5CR) (P5C reductase); pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (strain PAO); (M33557) delta-1-pyrroline-5-carboxylate reductase (EC 1.5.1.2) [Pseudomonas aeruginosa] (AL031740) 60s ribosomal protein l10a. [Schizosaccharomyces pombe]
16930	ENU00724	ANI61C5218: 34-66 1629..632	34-66	971-990	EST	"clc10a1.rl, clc10a1.fl"		252		2E-66			hypothetical 53.9 KD protein C1F5.08C in chromosome I; (Z68136) unknown [Schizosaccharomyces pombe]
16931	ENU00725	ANI61C1101 6:1959..961	28-49	964-984	EST	"n8e06a1.rl, n8e06a1.fl"		139		2E-32			probable serine/threonine-protein kinase C1D4.11C; (Z69239) unknown [Schizosaccharomyces pombe]
16932	ENU00726	ANI61C1027 7:6262..5262	22-46	961-980	EST	"z7f04a1.rl, z7f04a1.fl"		33		2.9			(AF027867) SacI methylase [Streptomyces achromogenes] (AF064070) putative epimerase/dehydratase WbiG [Burkholderia pseudomallei] hypothetical 89.2 KD protein C4H3.11C in chromosome I; (Z69380) unknown [Schizosaccharomyces pombe]
16933	ENU00727	ANI61C5890: 55-76 467..1472	55-76	997-1018	EST	"v7c05a1.rl, v7c05a1.fl"		32		5			ribosomal protein L12; 60S ribosomal protein L12; ribosomal protein L12 - human; (L06505) ribosomal protein L12 [Homo sapiens]
16934	ENU00728	ANI61C9978: 33-52 3494..2487	33-52	972-998	EST	"y4a06a1.rl, y4a06a1.fl"		36		0.57			(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
16935	ENU00729	ANI61C3947: 29-48 1493..485	29-48	967-995	EST	"x8b06a1.rl, x8b06a1.fl"		61		0.000000 01			
16936	ENU00730	ANI61C9564: 41-60 1335..325	41-60	982-1009	EST	"v7g01a1.rl, v7g01a1.fl"		147		2E-46			
16937	ENU00731	ANI50C7010 2_1:1444..432	24-44	967-994	EST	"c8f11a1.rl, c8f11a1.fl"		86		3E-17			
16938	ENU00732	ANI61C5415: 24-52 475..1494	24-52	982-1001	EST	"c8b03a1.rl, c8b03a1.fl"							

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16939	ENU00733	ANI61C5415: 475..1494	24-52	982-1001	EST	"o6e09a1.r1, o6e09a1.fl"		86	86	3E-17			(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
16940	ENU00734	ANI61C5415: 475..1494	24-52	982-1001	EST	"g2b05a1.r1, g2b05a1.fl"		86	86	3E-17			(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
16941	ENU00735	ANI61C6105: 1166..2186	22-47	974-1000	EST	"g7b11a1.r1, g7b11a1.fl"		131	131	6E-30			"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe] "
16942	ENU00736	ANI61C9555: 4102..5128	34-56	997-1016	EST	"m5c02a1.r1, m5c02a1.fl"		34	34	1.7			interleukin 4 receptor precursor; CD124 ; interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen) ; (X52425) interleukin 4 receptor [Homo sapiens] ; (AC004525) Interleukin 4 alpha-chain precursor [Homo sapiens]
16943	ENU00737	ANI61C8351: 4698..5725	29-52	987-1013	EST	"s9d01a1.r1, s9d01a1.fl"		92	92	2E-30			(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
16944	ENU00738	ANI61C4397: 2140..1113	22-52	988-1007	EST	"j9d05a1.r1, j9d05a1.fl"		39	39	0.039			aggregation protein asp1 - Enterococcus faecalis plasmid pPDI ; (X62656) aggregation substance (ASP1) [Enterococcus faecalis]
16945	ENU00739	ANI61C2666: 2876..3907	44-67	1013-1033	EST	"t2a05a1.r1, t2a05a1.fl"		32	32	5.1			light repressible receptor protein kinase - Arabidopsis thaliana ; (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]
16946	ENU00740	ANI61C8498: 102..1140	25-50	995-1021	EST	"r1d01a1.r1, r1d01a1.fl"		243	243	2E-63			(AL035216) probable involvement in ergosterol biosynthesis [Schizosaccharomyces pombe]
16947	ENU00741	ANI61C4920: 1676..637	32-51	996-1029	EST	"h8e02a1.r1, h8e02a1.fl"		335	335	e-121			"(S83228) beta-isopropylmalate dehydrogenase [Aspergillus niger, strain A733, Peptide, 363 aa] [Aspergillus niger] ; (U51130) beta-isopropylmalate dehydrogenase [Aspergillus niger] "

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16948	ENU00742	ANI61C8213: 22-42 915..1043		998-1022	EST	"y3h11a1.rl, y3h11a1.fl"			163	2E-39			"mitogen-activated protein kinase HOG1 (MAP kinase HOG1) (osmosensing protein HOG1) ; protein-kinase HOG1 (EC 2.7.1.-), mitogen-activated - yeast (Saccharomyces cerevisiae) ; (X89514) mitogen-activated protein kinase [Saccharomyces cerevisiae] ; (Z73285) ORF YLR113w [Saccharomyces cerevisiae]"
16949	ENU00743	ANI61C3025: 40-60 1503..459		1023-1042	EST	"m0h12a1.rl, m0h12a1.fl"			35	1			(D49835) DNA-binding protein [Homo sapiens]
16950	ENU00744	ANI61C7853: 22-54 1772..2821		994-1029	EST	"i7e03a1.rl, i7e03a1.fl"			32	8.9			(Z70755) weak similarity with xenopus XFIN protein (Swiss Prot accession number P08045) [Caenorhabditis elegans]
16951	ENU00745	ANI61C5148: 39-62 1660..609		1025-1047	EST	"f0f11a1.rl, f0f11a1.fl"			271	5E-85			(AF088906) clock-controlled gene-9 protein [Neurospora crassa]
16952	ENU00746	ANI61C331:2 34-53 38..1288		1022-1042	EST	"r5d11a1.rl, r5d11a1.fl"			36	0.46			(AC004138) unknown protein [Arabidopsis thaliana]
16953	ENU00747	ANI61C8247: 22-50 1551..2605		1010-1034	EST	"x7a08a1.rl, x7a08a1.fl"			36	0.6			(AC006528) putative mudrA transposase protein [Arabidopsis thaliana]
16954	ENU00748	ANI61C2872: 42-62 1221..165		1023-1056	EST	"j7c11a1.rl, j7c11a1.fl"			341	4E-93			"glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae]"
16955	ENU00749	ANI61C7556: 22-51 1231..2290		1004-1039	EST	"r4b04a1.rl, r4b04a1.fl"			33	3			(AF038614) contains similarity to Lentinula edodes MFBA=234.5 kda mature fruiting body adhesion protein (GB:S75826) [Caenorhabditis elegans]
16956	ENU00750	ANI61C9370: 66-87 176..1237		1058-1085	EST	"o8a11a1.rl, o8a11a1.fl"			136	5E-37			glutathione-dependent formaldehyde dehydrogenase (FDH) (FALDH) ; (L33464) alcohol dehydrogenase 3 [Methylobacter marinus]

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16957	ENU00751	ANI61C8056: 4476..3414	22-46	1007-1042	EST	"j0b08a1.rl, j0b08a1.fl"			108	2E-27			(AL031181) putative cell division involvement [Schizosaccharomyces pombe]; (AL035064) septin interacting protein homolog [Schizosaccharomyces pombe]
16958	ENU00752	ANI61C2678: 22-41 1085..2147	22-41	1011-1042	EST	"c7h03a1.rl, c7h03a1.fl"			95	6E-21			hypothetical 58.3 KD protein in PMT2-CCR4 intergenic region; FUN26 protein - yeast (Saccharomyces cerevisiae); (L05146) Fun26p [Saccharomyces cerevisiae]; (L05027) ORF YAL022 [Saccharomyces cerevisiae]
16959	ENU00753	ANI61C9359: 40-59 1978..3041	40-59	1027-1061	EST	"l0g11a1.rl, l0g11a1.fl"			157	2E-37			(AJ001414) GTPase activating protein [Yarrowia lipolytica]
16960	ENU00754	ANI61C9824: 65-87 3270..4335	65-87	1060-1088	EST	"c8a03a1.rl, c8a03a1.fl"			123	2E-27			(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]
16961	ENU00755	ANI61C60:35 29-52 97..2530	29-52	1023-1054	EST	"y4b09a1.rl, y4b09a1.fl"			34	1.4			(Z75539) predicted using Genefinder; cDNA EST EMBL:C13354 comes from this gene; cDNA EST EMBL:C11309 comes from this gene; cDNA EST yk477e3.3 comes from this gene; cDNA EST yk477e3.5 comes from this gene; cDNA EST yk462a1.3 comes...
16962	ENU00756	ANI61C2053: 25-60 1438..369	25-60	1027-1052	EST	"j9e12a1.rl, j9e12a1.fl"			319	2E-86			hypothetical 35.7 KD protein C26A3.11 in chromosome I; (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]
16963	ENU00757	ANI61C9659: 37-58 1356..278	37-58	1048-1073	EST	"c6c09a1.rl, c6c09a1.fl"			32	5.4			(AC007087) unknown protein [Arabidopsis thaliana]
16964	ENU00758	ANI61C7277: 47-68 2375..1297	47-68	1064-1083	EST	"d1d08a1.rl, d1d08a1.fl"			139	3E-32			(X92868) NADP-dependent alcohol dehydrogenase [Bacillus subtilis]; (Z99117) NADP-dependent alcohol dehydrogenase [Bacillus subtilis]
16965	ENU00759	ANI61C7087: 22-45 2146..1066	22-45	1025-1060	EST	"c4e01a1.rl, c4e01a1.fl"			128	8E-29			(AL023705) hypothetical protein [Schizosaccharomyces pombe]
16966	ENU00760	ANI61C4304: 54-73 1805..717	54-73	1065-1100	EST	"g6d09a1.rl, g6d09a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16967	ENU00761	ANI61C7147: 3274..4365	22-53	1041-1071	EST	"i3h06a1.rl", i3h06a1.fl"			492	e-138			calcium/calmodulin-dependent protein kinase (CMPK) ; Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans ; (M74120) calmodulin-dependent protein kinase [Emericella nidulans] ; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] ; thioredoxin H-type 2 (TRX-H2) ; thioredoxin h2 - common tobacco ; (Z11803) thioredoxin [Nicotiana tabacum] ; thioredoxin [Nicotiana tabacum]
16968	ENU00762	ANI61C8263: 25-44 1773..682	25-44	1054-1075	EST	"r1e01a1.rl", r1e01a1.fl"			34	2.4			(U95611) Cap1 [Candida albicans]
16969	ENU00763	ANI61C2172: 51-72 30..1130	51-72	1088-1109	EST	"y4e06a1.rl", y4e06a1.fl"			55	0.000000 9			(U28789) PACT [Mus musculus]
16970	ENU00764	ANI61C2654: 38-57 2689..1587	38-57	1078-1097	EST	"g3c02a1.rl", g3c02a1.fl"			38	0.12			ubiquitin-like protein 9 - Arabidopsis thaliana
16971	ENU00765	ANI61C3229: 22-45 820..1921	22-45	1054-1081	EST	"n8a02a1.rl", n8a02a1.fl"			117	6E-28			PRL1/PRL2-like protein ; (AB004535)
16972	ENU00766	ANI61C385:2 22-47 135..3237	22-47	1063-1082	EST	"i8d10a1.rl", i8d10a1.fl"			476	e-133			PRL1 [Schizosaccharomyces pombe]
16973	ENU00767	ANI61C1048 52-72 1:1932..3042	52-72	1086-1120	EST	"m7g04a1.rl", m7g04a1.fl"			33	3.2			(Z69368) unknown
16974	ENU00768	ANI61C3011: 64-83 3667..2551	64-83	1105-1139	EST	"w8e03a1.rl", w8e03a1.fl"			63	0.000000 004			[Schizosaccharomyces pombe]
16975	ENU00769	ANI61C1136: 27-48 6747..7865	27-48	1068-1103	EST	"f0g07a1.rl", f0g07a1.fl"							(U51566) ATF/CREB-family transcription factor [Schizosaccharomyces pombe]
16976	ENU00770	ANI61C6977: 40-60 1453..332	40-60	1091-1119	EST	"o8f01a1.rl", o8f01a1.fl"			142	2E-37			[Schizosaccharomyces pombe]
16977	ENU00771	ANI61C9177: 22-52 214..1342	22-52	1088-1108	EST	"d5h06a1.rl", d5h06a1.fl"			32	7.4			hypothetical protein YLR189c - yeast (Saccharomyces cerevisiae) ; (U17246)
16978	ENU00772	ANI61C2197: 71-89 3006..1873	71-89	1146-1165	EST	"k5h01a1.rl", k5h01a1.fl"			34	2.5			Ylr189cp [Saccharomyces cerevisiae] (X73888) cytochrome c [Escherichia coli]
													"(S82067) T-cell receptor beta chain variable region {C beta region} [human, melanoma-specific cytotoxic T-cell clone DT252 12-6C7, melanoma patient 252, Peptide Partial, 86 aa] [Homo sapiens]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16979	ENU00773	ANI61C9855: 2951..4097	59-78	1143-1163	EST	"l3g07a1.r1, l3g07a1.fl"			81	1E-14			(AL031852) hypothetical protein [Schizosaccharomyces pombe] (U18061) CAP20 [Glomerella cingulata]
16980	ENU00774	ANI61C632:5 41-71	41-71	1120-1147	EST	"r8b07a1.r1, r8b07a1.fl"			130	2E-29			(AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] (AB011822) clathrin light chain [Schizosaccharomyces pombe]
16981	ENU00775	ANI61C1086 43-64	43-64	1121-1152	EST	"q0e02a1.r1, q0e02a1.fl"			131	7E-30			"(Z98559) SPAC23C11.17; len:485aa, similar eg. to YPR125W, Q06493, chromosome xvi orf, (454aa), fasta scores, opt:1063, EQ:0, (43.5% identity in 418 aa overlap)
16982	ENU00776	ANI61C9103: 22-55	22-55	1113-1133	EST	"p0b11a1.r1, p0b11a1.fl"			66	7E-12			[Schizosaccharomyces pombe]
16983	ENU00777	ANI61C9039: 72-92	72-92	1152-1187	EST	"o8g08a1.r1, o8g08a1.fl"			275	5E-73			"(D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.] "
16984	ENU00778	ANI61C1093 44-65	44-65	1132-1159	EST	"f2f12a1.r1, f2f12a1.fl"			217	9E-56			unknown ; (AF075599) ubiquitin conjugating enzyme 12 [Homo sapiens] ; (AB012191) Nedd8-conjugating enzyme hUbc12 [Homo sapiens] (AB010900) YNL123w homolog [Schizosaccharomyces pombe]
16985	ENU00779	ANI61C1188: 22-51	22-51	1108-1138	EST	"g9h01a1.r1, g9h01a1.fl"			148	3E-48			PRP19-HSP104 intergenic region ; hypothetical protein YLL027w - yeast (Saccharomyces cerevisiae) ; (Z73132) ORF YLL027w [Saccharomyces cerevisiae]
16986	ENU00780	ANI61C1036 36-59	36-59	1133-1157	EST	"m5e02a1.r1, m5e02a1.fl"			222	5E-57			(AF094516) E1-like protein [Homo sapiens]
16987	ENU00781	ANI61C6804: 22-49	22-49	1125-1149	EST	"j0f02a1.r1, j0f02a1.fl"			138	1E-31			(AF104860) putative RNA-binding protein PRP-1 [Caenorhabditis elegans] "(AF045646) contains similarity to human cyclin A/CDK2-associated protein p19, an RNA polymerase II elongation factor-like protein (GB:U33760) [Caenorhabditis elegans]
16988	ENU00782	ANI61C6107: 24-59	24-59	1126-1152	EST	"c8c02a1.r1, c8c02a1.fl"			112	9E-27			"
16989	ENU00783	ANI61C3323: 67-85	67-85	1169-1195	EST	"x7b06a1.r1, x7b06a1.fl"			36	0.52			(AJ006350) polymerase [Duck hepatitis B virus]
16990	ENU00784	ANI61C893:1 23-49	23-49	1125-1153	EST	"t2h07a1.r1, t2h07a1.fl"			34	0.0008			
16991	ENU00785	ANI61C8934: 31-50	31-50	1134-1162	EST	"x8c05a1.r1, x8c05a1.fl"			35	1.2			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16992	ENU00786	ANI61C1135	68-93	1176-1200	EST	"i7e08a1.r1, i7e08a1.fl"		53	0.000003				(AL034490) putative tyrosine kinase [Schizosaccharomyces pombe]
16993	ENU00787	8:1793..2967 ANI61C3480: 3144..1961	22-55	1140-1163	EST	"o8d09a1.r1, o8d09a1.fl"		33	4.6				acrosomal protein AZ1 - mouse ; (D43921) pre-acrosome localization protein [Mus musculus] ; (D88509) AZ-1 [Mus musculus] (AF050672) ribosomal protein L13E [Candida albicans] ; (AL033497) ribosomal protein L13e [Candida albicans] ; (U80854) ribosomal protein L13 [Candida albicans] (AF083325) phosphatase-like protein [Homo sapiens] "(AB000628) UDP-GlcNAc: a-1,3-D - mannoside b-1,4-N-Acetylglucosaminyltransferase IV [Bos taurus]"
16994	ENU00788	ANI61C9543: 2435..1249	45-64	1158-1189	EST	"w9a11a1.r1, w9a11a1.fl"		68	3E-23				
16995	ENU00789	ANI61C1064 4:3051..4241	68-87	1184-1215	EST	"h4e03a1.r1, h4e03a1.fl"		41	0.021				
16996	ENU00790	ANI61C3465: 1756..566	28-51	1142-1177	EST	"e0b10a1.r1, e0b10a1.fl"		43	0.004				
16997	ENU00791	ANI61C9562: 520..1713	52-72	1182-1202	EST	"g5c09a1.r1, g5c09a1.fl"		189	3E-55				GTP-binding protein SARA ; (Z67742) sarA [Aspergillus niger]
16998	ENU00792	ANI61C6956: 339..1538	26-45	1161-1183	EST	"r2b05a1.r1, r2b05a1.fl"		157	2E-37				(X99853) oxoglutarate malate translocator [Solanum tuberosum]
16999	ENU00793	ANI61C2326: 1236..32	27-47	1168-1189	EST	"r5e09a1.r1, r5e09a1.fl"		45	0.001				(AL023634) hypothetical protein [Schizosaccharomyces pombe]
17000	ENU00794	ANI61C6814: 4189..2970	22-42	1169-1199	EST	"f0a12a1.r1, f0a12a1.fl"		122	5E-27				hypothetical 32.6 KD protein in VPS15-YMC2 intergenic region ; hypothetical protein YBR101c - yeast (Saccharomyces cerevisiae) ; (X78993) YBR0830 [Saccharomyces cerevisiae] ; (Z35970) ORF YBR101c [Saccharomyces cerevisiae]
17001	ENU00795	ANI61C7104: 2817..1597	22-56	1167-1200	EST	"n8e07a1.r1, n8e07a1.fl"		60	3E-18				"RNase Irl=base non-specific acid ribonuclease [Irlpex lacteus, Peptide, 250 aa]"
17002	ENU00796	ANI61C6919: 2563..1338	24-43	1172-1207	EST	"n0b06a1.r1, n0b06a1.fl"		322	5E-94				aminopeptidase Y (EC 3.4.11.-) precursor - yeast (Saccharomyces cerevisiae)
17003	ENU00797	ANI61C3368: 7084..8312	30-49	1186-1216	EST	"g3b06a1.r1, g3b06a1.fl"		437	e-122				(AL033385) transketolase [Schizosaccharomyces pombe]
17004	ENU00798	ANI61C4572: 3705..2471	53-72	1214-1244	EST	"m0d06a1.r1, m0d06a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17005	ENU00799	ANI61C1536: 2827..4066	22-54	1200-1219	EST	"d5b01a1.r1, d5b01a1.fl"		36	0.72				inhibitory regulator protein IRA2 ; (M33779) IRA2 protein (IRA2) [Saccharomyces cerevisiae]
17006	ENU00800	ANI61C9250: 1679..440	26-61	1194-1223	EST	"d3f01a1.r1, d3f01a1.fl"		244	8E-64				probable NADP-dependent oxidoreductase P1 ; zeta-crystallin homolog - Arabidopsis thaliana ; (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
17007	ENU00801	ANI61C9202: 2072..3324	22-48	1213-1232	EST	"o8f12a1.r1, o8f12a1.fl"		226	e-118				ubiquitin--protein ligase RSP5 ; hypothetical protein YER125w - yeast (Saccharomyces cerevisiae) ; (U18916) Rsp5p [Saccharomyces cerevisiae]
17008	ENU00802	ANI61C1055 7:2994..4251	22-54	1204-1237	EST	"g9e09a1.r1, g9e09a1.fl"		125	2E-30				"NADH-cytochrome B5 reductase precursor (P34/P32) ; cytochrome-b5 reductase (EC 1.6.2.2), mitochondrial outer membrane form - yeast (Saccharomyces cerevisiae) ; (Z26877) unknown [Saccharomyces cerevisiae] ; (Z28150) ORF YKL150w [Saccharomyces cerevisiae] ; (X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] "
17009	ENU00803	ANI61C6800: 2631..1372	31-51	1221-1248	EST	"g5d10a1.r1, g5d10a1.fl"		72	7E-12				nuclear protein SON1 (UB fusion degradation protein 5) ; nuclear protein SON1 - yeast (Saccharomyces cerevisiae) ; (L00928) nuclear protein [Saccharomyces cerevisiae] ; (Z48432) nuclear protein SON1 (L00928) [Saccharomyces cerevisiae] ; (Z74068) ORF YDL020c [Saccharomyces cerevisiae]
17010	ENU00804	ANI61C5194: 1603..335	49-68	1242-1275	EST	"d1h08a1.r1, d1h08a1.fl"		128	1E-58				40S ribosomal protein S4 (omnipotent suppressor protein SUP44) (RP12) (S2E) ; ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) ; (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] ; (Z72645) ORF YGL123w [Saccharomyces cerevisiae] ; (X94106) SUP44 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17011	ENU00805	ANI61C6105: 868..2147	38-57	1252-1275	EST	"d3a07a1.rl, d3a07a1.fl"		220	220	2E-56			"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe] "
17012	ENU00806	ANI61C1430: 22-51 5544..6828	22-51	1241-1264	EST	"d3b03a1.rl, d3b03a1.fl"		197	197	8E-74			(AL021730) hypothetical protein [Schizosaccharomyces pombe]
17013	ENU00807	ANI61C7432: 22-43 640..1925	22-43	1233-1265	EST	"t2d09a1.rl, t2d09a1.fl"		34	34	1.7			[Z94043] hypothetical protein [Bacillus subtilis] ; (Z99121) alternate gene name: yzkA; similar to cell wall-binding protein [Bacillus subtilis]
17014	ENU00808	ANI61C1065 50-71 4:2016..726	50-71	1279-1298	EST	"k0h11a1.rl, k0h11a1.fl"		98	98	1E-19			probable glucose transporter RCO-3 ; (U54768) RCO3 [Neurospora crassa]
17015	ENU00809	ANI61C6107: 33-53 3106..4399	33-53	1259-1284	EST	"r7c07a1.rl, r7c07a1.fl"		108	108	1E-58			(AL022103) deoxycytidylate deaminase [Schizosaccharomyces pombe]
17016	ENU00810	ANI61C9185: 28-51 2399..1101	28-51	1254-1284	EST	"m5f03a1.rl, m5f03a1.fl"		94	94	7E-33			(U22463) T-2 toxin biosynthesis protein; tri7 [Fusarium sporotrichioides]
17017	ENU00811	ANI61C289:3 22-50 229..1930	22-50	1254-1279	EST	"r7f07a1.rl, r7f07a1.fl"		324	324	8E-88			"(S66039) NAD(+)-specific glutamate dehydrogenase, NAD-GDH {EC 1.4.1.2} [Neurospora crassa, Peptide, 1047 aa] [Neurospora crassa] ; Glu dehydrogenase [Neurospora crassa] "
17018	ENU00812	ANI61C7273: 35-55 3807..2486	35-55	1280-1314	EST	"k5g01a1.rl, k5g01a1.fl"		87	87	5E-20			"hypothetical 23.0 KD protein C3F10.12C in chromosome I ; (Z69369) SPAC3F10.12c, unknown, 201, similar to transcription factors and SW:CBF1_YEAST P17106 centromere-binding protei n 1 (39.8% identity in 113 aa overlap), contains PS00038 Myc-type, 'helix-loop-helix' dimerization dom..."
17019	ENU00813	ANI61C8229: 63-84 840..2170	63-84	1321-1351	EST	"t2b02a1.rl, t2b02a1.fl"		34	34	2.3			hypothetical 73.3 KD protein C6G9.14 in chromosome I ; (Z81317) serine rich pumilio family rna binding domain protein [Schizosaccharomyces pombe]
17020	ENU00814	ANI61C8716: 22-50 4027..2695	22-50	1281-1312	EST	"z1c12a1.rl, z1c12a1.fl"		34	34	2.3			(U78551) mucin MUC5B [Homo sapiens]

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17021	ENU00815	ANI50C1117 4_1:1679..307	37-59	1331-1352	EST	"b0g03a1.r1, b0g03a1.fl"		102	2E-38				DNA-directed RNA polymerase II 19 KD polypeptide ; (D86554) RNA polymerase II subunit Rpb7 [Schizosaccharomyces pombe] ; (D89594) RNA polymerase II subunit Rpb7 [Schizosaccharomyces pombe] ; (AF027821) Rpb7 [Schizosaccharomyces pombe] ; (AF055916) RNA polymerase II subunit Rpb7 [Schizosaccharomyces pombe] "probable arginyl-TRNA synthetase, cytoplasmic (arginine--TRNA ligase) (ARGRS) ; probable arginine--tRNA ligase (EC 6.1.1.19) - yeast (Saccharomyces cerevisiae) ; (U51032) Ydr341cp [Saccharomyces cerevisiae] "
17022	ENU00816	ANI61C1037 4:1210..2584	37-59	1339-1369	EST	"r1a02a1.r1, r1a02a1.fl"		199	e-113				(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus] HPBR11-7 protein - human ; (X67337) Human pre-mRNA cleavage factor I 68 kDa subunit [Homo sapiens] ; (X67336) HPBR11-7 [Homo sapiens] hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae) ; (Z75105) ORF YOR197w [Saccharomyces cerevisiae] Repressible alkaline phosphatase precursor ; alkaline phosphatase (EC 3.1.3.1) - yeast (Saccharomyces cerevisiae) ; (U33050) Pho8p: repressible alkaline phosphatase; CAI: 0.16 [Saccharomyces cerevisiae] (AL031743) putative protein transport protein [Schizosaccharomyces pombe]
17023	ENU00817	ANI61C2914: 20..1402	41-61	1353-1381	EST	"o0d06a1.r1, o0d06a1.fl"		741	0				
17024	ENU00818	ANI61C3137: 161..1	28-49	1372-1396	EST	"t2h11a1.r1, t2h11a1.fl"		43	0.007				
17025	ENU00819	ANI61C8615: 539..1951	54-73	1400-1424	EST	"e0g10a1.r1, e0g10a1.fl"		353	2E-96				
17026	ENU00820	ANI61C9379: 1868..447	40-59	1389-1417	EST	"j0g12a1.r1, j0g12a1.fl"		233	3E-64				
17027	ENU00821	ANI61C3740: 88..1508	55-75	1411-1434	EST	"j9c11a1.r1, j9c11a1.fl"		201	1E-50				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17028	ENU00822	ANI61C9283: 5828..4401	22-57	1372-1407	EST	"d3b06a1.rl, d3b06a1.fl"		87	87	3E-16			"mitochondrial acidic protein MAM33 precursor ; hypothetical protein YIL070c - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]"
17029	ENU00823	ANI61C9283: 5839..4401	24-43	1385-1420	EST	"p0e09a1.rl, p0e09a1.fl"		87	87	3E-16			"mitochondrial acidic protein MAM33 precursor ; hypothetical protein YIL070c - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]"
17030	ENU00824	ANI61C9283: 5828..4381	22-57	1394-1427	EST	"x9c12a1.rl, x9c12a1.fl"		87	87	3E-16			"mitochondrial acidic protein MAM33 precursor ; hypothetical protein YIL070c - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]"
17031	ENU00825	ANI61C5338: 743..567	23-50	1394-1429	EST	"p0c02a1.rl, p0c02a1.fl"		100	100	3E-23			(AL023518) hypothetical protein [Schizosaccharomyces pombe]
17032	ENU00826	ANI61C1649: 2395..941	42-61	1420-1454	EST	"g5c04a1.rl, g5c04a1.fl"		217	217	2E-55			probable serine/threonine-protein kinase C29A4.16 ; (Z97210) protein kinase [Schizosaccharomyces pombe]
17033	ENU00827	ANI61C8443: 4202..2748	22-46	1411-1434	EST	"d5a07a1.rl, d5a07a1.fl"		282	282	4E-77			type II proteins geranylgeranyltransferase beta subunit (type II protein geranyl-geranyltransferase beta subunit) (GGTase-II-beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta subunit) ; probable protein prenyltransferase (EC 2.5.1.-) BET2 - yeast (Saccharomyces cerevisiae) ; (U25842) Protein Geranyl-geranyltransferase beta subunit (Swiss Prot. accession number P20133; P32433) [Saccharomyces cerevisiae]
17034	ENU00828	ANI61C7625: 1891..409	40-59	1443-1468	EST	"g6c08a1.rl, g6c08a1.fl"		51	51	0.00002			(Z46970) secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]
17035	ENU00829	ANI61C7625: 1891..409	40-59	1443-1468	EST	"d3g05a1.rl, d3g05a1.fl"		51	51	0.00002			(Z46970) secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17036	ENU00830	ANI61C9270: 2951..1463	54-73	1465-1500	EST	"c7f12a1.r1, c7f12a1.fl"		70	236	3E-11			(AF039217) inv candidate homolog [Homo sapiens] "Succinic semialdehyde dehydrogenase ; (Y111192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] ; (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens]"
17037	ENU00831	ANI61C2972: 4977..3488	53-72	1466-1499	EST	"j4g02a1.r1, j4g02a1.fl"							26S protease regulatory subunit 6A homolog (TAT-binding protein homolog 1) (TBP-1) ; (D88663) Tat binding protein 1 [Brassica rapa] probable serine/threonine-protein kinase C29A4.16 ; (Z97210) protein kinase [Schizosaccharomyces pombe]
17038	ENU00832	ANI61C1086 22-45 6:1100..2594	22-45	1441-1474	EST	"o8g12a1.r1, o8g12a1.fl"		344		e-151			arginine permease; arginine transport protein - yeast (Saccharomyces cerevisiae) ; (M11724) amino acid permease [Saccharomyces cerevisiae] ; (U18795) Can1p: arginine permease [Saccharomyces cerevisiae]
17039	ENU00833	ANI61C1649: 2416..896	54-73	1511-1532	EST	"g6g06a1.r1, g6g06a1.fl"		217		2E-55			(U77605) two-component histidine kinase CHK-1 [Glomerella cingulata] ; (U77606) two-component histidine kinase CHK-1 [Glomerella cingulata] (M16076) low temperature essential protein [Saccharomyces cerevisiae]
17040	ENU00834	ANI61C2242: 4904..3363	29-48	1499-1527	EST	"w7b01a1.r1, w7b01a1.fl"		146		1E-95			probable membrane protein YDR105c-yeast (Saccharomyces cerevisiae) ; (Z47746) unknown [Saccharomyces cerevisiae] ; (Z48758) unknown [Saccharomyces cerevisiae]
17041	ENU00835	ANI61C9231: 733..2284	66-86	1550-1575	EST	"d5c12a1.r1, d5c12a1.fl"		90		6E-29			hypothetical protein YDR330w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr330wp [Saccharomyces cerevisiae]
17042	ENU00836	ANI61C1103 67-88 3:4042..5596	67-88	1544-1579	EST	"w7h10a1.r1, w7h10a1.fl"		157		1E-37			3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA-reductase [Gibberella fujikuroi]
17043	ENU00837	ANI61C3573: 3114..1551	43-63	1540-1564	EST	"i0h03a1.r1, i0h03a1.fl"		195		3E-80			
17044	ENU00838	ANI61C1048 55-78 2:1783..214	55-78	1562-1582	EST	"d3c06a1.r1, d3c06a1.fl"		159		5E-38			
17045	ENU00839	ANI61C9735: 2323..754	65-84	1557-1592	EST	"q0d11a1.r1, q0d11a1.fl"		411		e-158			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17046	ENU00840	ANI61C1122 9:1380..2970	26-50	1539-1574	EST	"j0d08a1.r1, j0d08a1.fl"		151	1E-35				probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae) ; (Z74122) ORF YDL074c [Saccharomyces cerevisiae]
17047	ENU00841	ANI61C9431: 31-51 997..2601	31-51	1563-1593	EST	"c8a01a1.r1, c8a01a1.fl"		247	1E-64				hypothetical 73.3 KD protein C6G9.14 in chromosome I ; (Z81317) serine rich pumilio family rna binding domain protein [Schizosaccharomyces pombe]
17048	ENU00842	ANI61C2435: 27-50 2495..888	27-50	1568-1592	EST	"y6e09a1.r1, y6e09a1.fl"		213	8E-64				"(D89173) similar to Saccharomyces cerevisiae hypothetical 36.4KD protein in SOD1-CPA2 intergenic region, SWISS-PROT Accession Number P47143 [Schizosaccharomyces pombe] ; (AL023781) adenosine kinase [Schizosaccharomyces pombe] " (AB004535) BEM46 protein [Schizosaccharomyces pombe]
17049	ENU00843	ANI61C6294: 23-48 1092..2726	23-48	1581-1615	EST	"r2d07a1.r1, r2d07a1.fl"		58	0.000000	2			[Schizosaccharomyces pombe] (AJ001836) fumarylacetoacetate hydrolase [Emmericella nidulans]
17050	ENU00844	ANI61C3681: 56-75 2484..2906	56-75	1621-1648	EST	"d3e01a1.r1, d3e01a1.fl"		129	3E-40				(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
17051	ENU00845	ANI61C1021 42-61 3:146..1781	42-61	1606-1635	EST	"r6e06a1.r1, r6e06a1.fl"		62	0.000000	01			hydroxylase [Streptomyces coelicolor] (U43775) secreted aspartic proteinase precursor [Glomerella cingulata]
17052	ENU00846	ANI61C4412: 22-49 8068..6409	22-49	1604-1639	EST	"k5g08a1.r1, k5g08a1.fl"		226	9E-76				(X00528) URF c-ras (sc-2) [Saccharomyces cerevisiae]
17053	ENU00847	ANI61C1073 23-42 5:82..1774	23-42	1639-1673	EST	"i3e07a1.r1, i3e07a1.fl"		87	4E-16				PRL1/PRL2-like protein ; (AB004535)
17054	ENU00848	ANI61C385:3 27-49 855..2149	27-49	1663-1691	EST	"i8f02a1.r1, i8f02a1.fl"		516	e-145				PRL1 [Schizosaccharomyces pombe] (AF009418) trichothecene biosynthesis transcription factor [Myrothecium roridum]
17055	ENU00849	ANI61C6251: 43-62 7770..9499	43-62	1704-1730	EST	"w4h05a1.r1, w4h05a1.fl"		38	0.16				(Y13700) MEAB protein [Emmericella nidulans]
17056	ENU00850	ANI61C1115 22-44 9:5337..3601	22-44	1697-1716	EST	"k5b02a1.r1, k5b02a1.fl"		35	0.45				RNA helicase [Schizosaccharomyces pombe]
17057	ENU00851	ANI61C9577: 27-46 1769..31	27-46	1703-1723	EST	"h1c03a1.r1, h1c03a1.fl"		153	8E-68				(Z99759) hypothetical protein [Schizosaccharomyces pombe]
17058	ENU00852	ANI61C8358: 25-47 2055..294	25-47	1709-1744	EST	"f0e12a1.r1, f0e12a1.fl"		46	6E-13				retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 ; (X13291) polyprotein [Arabidopsis thaliana]
17059	ENU00853	ANI61C3679: 22-52 5806..4045	22-52	1709-1741	EST	"g9e10a1.r1, g9e10a1.fl"		156	6E-40				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17060	ENU00854	ANI61C8625: 4677..2877	25-44	1748-1783	EST	"k5e01a1.rl, k5e01a1.fl"			520	0			"(AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe]" (Z99120) similar to acylaminoacyl-peptidase [Bacillus subtilis] (AF117876) malate dehydrogenase [Vibrio cholerae] "Arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) ; (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger] ; endo-1,5-alpha-L-arabinase [Aspergillus niger]" (U38191) protein phosphatase 2A0 B' regulatory subunit beta3 isoform [Oryctolagus cuniculus] ; protein phosphatase 2A:subunit=B'isotype=beta3 [Oryctolagus cuniculus]
17061	ENU00855	ANI61C380:3 55-74	55-74	1860-1887	EST	"g3e05a1.rl, g3e05a1.fl"			64	0.000000			
17062	ENU00856	ANI61C9368: 49-68	49-68	1878-1900	EST	"c8g06a1.rl, c8g06a1.fl"			39	0.1			
17063	ENU00857	ANI61C1007: 59-80	59-80	1892-1911	EST	"o0g06a1.rl, o0g06a1.fl"			217	2E-55			
17064	ENU00858	ANI61C8161: 1864..3782	26-52	1878-1901	EST	"m5b10a1.rl, m5b10a1.fl"			243	3E-63			
17065	ENU00859	ANI61C8056: 22-48	22-48	1913-1940	EST	"k5e03a1.rl, k5e03a1.fl"			153	1E-66			"probable malate dehydrogenase, mitochondrial precursor ; (AF002197) Similar to malate dehydrogenase; coded for by C. elegans cDNA cm7d6; coded for by C. elegans cDNA yk167g11.5; coded for by C. elegans cDNA cm15d12; coded for by C. elegans cDNA yk139h4.5; coded for by C. elegans cDNA yk169h8.5; co.."
17066	ENU00860	ANI61C9304: 43-70	43-70	1972-1995	EST	"w7f03a1.rl, w7f03a1.fl"			50	0.000000			probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae]
17067	ENU00861	ANI61C1065 4:5196..4758	25-49	1957-1988	EST	"i0c04a1.rl, i0c04a1.fl"			52	0.00001			[Arabidopsis thaliana] (AF049236) unknown [Arabidopsis thaliana]
17068	ENU00862	ANI61C1094 4:106..2136	35-54	2000-2023	EST	"p0h02a1.rl, p0h02a1.fl"			94	3E-18			MAP-homologous protein 1 ; microtubule-interacting protein MHP1 - yeast (Saccharomyces cerevisiae) ; (Z49317) ORF YJL042w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17069	ENU00863	ANI61C9558: 19..2128	40-59	2085-2107	EST	"g8b01a1.r1, g8b01a1.fl"			64	0.000000	003		prostaglandin G/H synthase 2 precursor (cyclooxygenase -2) (COX-2)
													(prostaglandin-endoperoxide synthase 2) (prostaglandin H2 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II) ; (U97696) cyclooxygenase-2 [Oryctolagus cuniculus]
17070	ENU00864	ANI61C5339: 7838..5616	27-54	2184-2207	EST	"w7h02a1.r1, w7h02a1.fl"			37	0.47			(M88172) ORF2 [Saccharomyces cerevisiae]
17071	ENU00865	ANI61C1097: 4:6218..5884	22-54	2211-2236	EST	"r4c11a1.r1, r4c11a1.fl"			35	1.8			(M16724) Ig H-chain V-region [Mus musculus]
17072	ENU00866	ANI61C5266: 1524..3839	22-54	2268-2295	EST	"i3a02a1.r1, i3a02a1.fl"			674	0			phosphoenolpyruvate carboxykinase [ATP] ; (U38575)
													phosphoenolpyruvate carboxykinase [Kluveromyces lactis]
17073	ENU00867	ANI61C4810: 35..2379	56-75	2323-2358	EST	"c8g07a1.r1, c8g07a1.fl"			478	e-134			PHO85 protein - yeast (Saccharomyces cerevisiae) ; (U43503) Lph16p [Saccharomyces cerevisiae]
17074	ENU00868	ANI61C2582: 2273..4664	47-67	2362-2395	EST	"i7b04a1.r1, i7b04a1.fl"			869	0			probable ATP-dependent transporter YER036C ; hypothetical protein YER036c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer036cp [Saccharomyces cerevisiae]
17075	ENU00869	ANI61C2959: 980..3469	38-55	2464-2485	EST	"f2f10a1.r1, f2f10a1.fl"			94	5E-18			"ribosome receptor, 180k - dog ; (X87224) ribosome receptor [Canis familiaris]"
17076	ENU00870	ANI61C2609: 4010..1336	45-64	2647-2677	EST	"y4h10a1.r1, y4h10a1.fl"			39	0.11			zinc finger protein MSN2 (multicopy suppressor of SNF1 protein 2) ; finger protein MSN2 - yeast (Saccharomyces cerevisiae) ; (L08838) zinc finger protein [Saccharomyces cerevisiae] ; (Z48502) Msn2p [Saccharomyces cerevisiae]
17077	ENU00871	ANI61C8923: 14..2838	31-55	2778-2813	EST	"v7h12a1.r1, v7h12a1.fl"			95	2E-18			(Y09899) hypothetical protein [Calothrix viguieri]
17078	ENU00872	ANI61C5853: 2734..2542	22-45	153-180	EST	"c9g08a1.r1, c9g08a1.fl"		749	36	0.06			(X60288) medium chains of clathrin associated protein complex [Saccharomyces cerevisiae]
17079	ENU00873	ANI61C4443: 1..1009	22-43	749-771	EST	"h4e12a1.r1, h4e12a1.fl"		1069					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17080	ENU00874	ANI61C2796: 1099..555	112-131	477-496	EST	"m8c12a1.rl, m8c12a1.fl"		1371	60	0.000000	01		Molybdopter biosynthesis MOEA protein ; (X99625) moeA [Synechococcus sp.]
17081	ENU00875	ANI61C9928: 968..780	22-47	173-198	EST	"e9c10a1.rl, e9c10a1.fl"		694	56	0.000000	07		(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
17082	ENU00876	ANI61C7486: 3341..3090			EST	"b0f07a1.rl, b0f07a1.fl"		902	148	2E-35			cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
17083	ENU00877	ANI61C5317: 3198..2946			EST	"g7a10a1.rl, g7a10a1.fl"		1140	39	0.008			"(AF106583) contains similarity to electron transfer flavoprotein beta (Pfam: PF01012, Score=278.7, E=7.6e-80, N=1) [Caenorhabditis elegans] "
17084	ENU00878	ANI61C4978: 4589..3141	22-47	808-829	EST	"o0b05a1.rl, o0b05a1.fl"		2014	33	3.1			(AE001428) predicted integral membrane protein [Plasmodium falciparum]
17085	ENU00879	ANI61C4126: 1849..3657	24-43	801-828	EST	"n3f03a1.rl, n3f03a1.fl"		2230	284	5E-76			Plasma membrane ATPase (proton pump) ; (L07305) ATPase [Ajellomyces capsulatus] ; H ATPase [Ajellomyces capsulatus]
17086	ENU00880	ANI61C6585: 187..1301	22-48	802-829	EST	"y6c06a1.rl, y6c06a1.fl"		2321	213	1E-62			40S ribosomal protein SA homolog (ribosome-associated protein 1) ; (U36470) putative ribosome-associated protein [Neurospora crassa]
17087	ENU00881	ANI61C2344: 2313..1554	30-49	716-739	EST	"r5d10a1.rl, r5d10a1.fl"		5376	42	0.004			(AL023706) small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
17088	ENU00882	ANI61C7644: 671..1661	22-45	716-740	EST	"g4a08a1.rl, g4a08a1.fl"		2375	34	1			(AF053614) dorsal B [Drosophila melanogaster]
17089	ENU00883	ANI61C7757: 875..1999	33-54	631-658	EST	"l0e12a1.rl, l0e12a1.fl"		3986	55	0.000000	5		(Z98269) EG:87B1.6 [Drosophila melanogaster]
17090	ENU00884	ANI61C3006: 472..132	31-48	459-479	EST	"t2h02a1.rl, t2h02a1.fl"		1218	36	0.23			(L16975) alpha-acetolactate synthase [Lactococcus lactis]
17091	ENU00885	ANI61C8082: 968..2224	29-50	807-829	EST	"w4h08a1.rl, w4h08a1.fl"		2888	89	5E-17			(AJ001726) complex I intermediate associated protein CIA35 [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17092	ENU00886	ANI61C9138: 1..403	192-215	355-382	EST	"z5g05a1.r1, z5g05a1.fl"		1434	31	3.3			TANKYRase ; (AF082556) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]
17093	ENU00887	ANI61C1062 46-66	779-803		EST	"g6c02a1.r1, g6c02a1.fl"		1671					genome polyprotein [contains: coat proteins VP1 TO VP4; core proteins P2A TO P2C; probable proteins P3A TO P3C; RNA-directed RNA polymerase P3D] ; genome
17094	ENU00888	ANI61C5632: 22-44 5336..5794	366-385		EST	"t2a07a1.r1, t2a07a1.fl"		1840	34	0.9			polyprotein - simian hepatitis A virus (strain AGM-27) ; (D00924)
17095	ENU00889	ANI61C1047 4:1681..1526			EST	"x7c05a1.r1, x7c05a1.fl"		622	30	2.7			polyprotein [Simian hepatitis A virus] hypothetical protein UL42 ; hypothetical protein UL42 - human cytomegalovirus (strain AD169) ; (X17403) HCMVUL42 [human herpesvirus 5]
17096	ENU00890	ANI61C4449: 55-73 795..153	595-622		EST	"j4e03a1.r1, j4e03a1.fl"		1476	36	0.19			(AB011182) KIAA0610 protein [Homo sapiens]
17097	ENU00891	ANI61C1232: 26-45 12838..7822	803-823		EST	"y3f11a1.r1, y3f11a1.fl"		1921	47	0.0002			(L35053) homolog of retroviral gag genes; putative [Magnaporthe grisea]
17098	ENU00892	ANI61C9271: 27-48 750..2417	778-805		EST	"v7a11a1.r1, v7a11a1.fl"		1510	36	0.35			"mucin 2 precursor, intestinal - human (fragments) "
17099	ENU00893	ANI61C9708: 22-49 2350..2833	453-479		EST	"o6a04a1.r1, o6a04a1.fl"		3942	32	2.7			"leucyl-tRNA synthetase, cytoplasmic (leucine--tRNA ligase) (LEURS) ; leucine--tRNA ligase (EC 6.1.1.4), cytosolic - Neurospora crassa ; (M30473) leucyl-tRNA synthetase [Neurospora crassa] "
17100	ENU00894	ANI61C1372: 63-82 2240..2084	379-406		EST	"f0h08a1.r1, f0h08a1.fl"		586	31	7.8			(U30905) mod2.2 [Drosophila melanogaster]
17101	ENU00895	ANI61C440:1 28-55 404..1883	458-479		EST	"y6a07a1.r1, y6a07a1.fl"		1697	31	4.6			(AB010636) SADH [Candida parapsilosis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17102	ENU00896	ANI61C7521: 1..266	42-61	184-203	EST	"o8e01a1.r1, o8e01a1.fl"		947	32	0.89			cytochrome C oxidase polypeptide VI precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Saccharomyces cerevisiae) ; (M10138) cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] ; (U00062) Cox6p: cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] beta-hexosaminidase precursor (N-acetyl-beta-glucosaminidase) (beta-GLCNACase) (beta-N-acetylhexosaminidase) hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] histone H1 ; histone H1 - yeast (Saccharomyces cerevisiae) ; (U43703) Lpl17p [Saccharomyces cerevisiae] "isopenicillin N synthetase (IPNS) ; isopenicillin N synthase (EC 1.-.-.-) - Emericella nidulans ; Chain A, Isopenicillin N Synthase From Aspergillus Nidulans (Manganese Complex) ; Isopenicillin N Synthase From Aspergillus Nidulans (Acv-Fe-No Complex) ; Isopenicillin N Synthase From Aspergillus Nidulans (Acv-Fe Complex) ; (M21882) isopenicillin N synthetase [Emericella nidulans] ; (M1811) isopenicillin N synthetase [Emericella nidulans] ; isopenicillin N synthetase [Emericella nidulans] "
17103	ENU00897	ANI61C7493: 839..1	25-44	793-818	EST	"o9a11a1.r1, o9a11a1.fl"		1362	273	1E-72			
17104	ENU00898	ANI61C1683: 1577..347	22-48	789-816	EST	"l3e10a1.r1, l3e10a1.fl"		1667	123	1E-27			
17105	ENU00899	ANI61C4586: 1161..1	22-46	726-753	EST	"x7d08a1.r1, x7d08a1.fl"		4544	46	0.0002			
17106	ENU00900	ANI61C291:2 918..3081	22-49	434-461	EST	"q0c04a1.r1, q0c04a1.fl"		602	240	4E-63			
17107	ENU00901	ANI61C3610: 1..106			EST	"k0c09a1.r1, k0c09a1.fl"		388					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17108	ENU00902	ANI61C7523: 22-48 2791..2602			EST	"a0g08a1.r1, a0g08a1.fl"		718	59	0.000000 02			(U40945) coded for by <i>C. elegans</i> cDNA yk74b9.3; coded for by <i>C. elegans</i> cDNA yk74b9.5; similar to repeat of calcium channel alpha subunits; similar to tetracycline resistance protein; similar to hypothetical protein in HSP30-PMP1 region (SP... (Z68115) F19H6.3 [<i>Caenorhabditis elegans</i>]
17109	ENU00903	ANI61C297:7 28-55 304..8452	772-798		EST	"m5c12a1.r1, m5c12a1.fl"		1268	34	1.4			Versicolorin reductase ; (U34740) putative ketoreductase [<i>Emmericella nidulans</i>]
17110	ENU00904	ANI61C1233: 71-95 938..1276	421-448		EST	"g8d01a1.r1, g8d01a1.fl"		1164					Diphthine synthase (diphthamide biosynthesis methyltransferase) ; methytransferase DPH5 - yeast (<i>Saccharomyces cerevisiae</i>) ; (M83375) DPH5 [<i>Saccharomyces cerevisiae</i>] ; (U17246) Dph5p: diphthine synthase [<i>Saccharomyces cerevisiae</i>] (U80437) coded for by <i>C. elegans</i> cDNA yk126f1.5 [<i>Caenorhabditis elegans</i>] kinesin-like protein KLPA ; kinesin-related protein KLPA - <i>Emmericella nidulans</i> ; (X64603) KLPA [<i>Emmericella nidulans</i>]
17111	ENU00905	ANI61S1679: 106-127 1..674	438-464		EST	"z4b06a1.r1, z4b06a1.fl"		3725	273	1E-72			
17112	ENU00906	ANI61C6471: 28-55 5890..4840	786-813		EST	"s9d11a1.r1, s9d11a1.fl"		2414	284	7E-76			
17113	ENU00907	ANI61C4735: 24-43 701..1976	771-790		EST	"t2a06a1.r1, t2a06a1.fl"		2094	32	5.3			
17114	ENU00908	ANI61C5578: 32-51 1582..1058	482-504		EST	"q0b12a1.r1, q0b12a1.fl"		1506	116	8E-26			
17115	ENU00909	ANI61C8897: 1..171			EST	"y6c03a1.r1, y6c03a1.fl"		508					(AL023706) apoptosis specific protein homologue [<i>Schizosaccharomyces pombe</i>] (AL049522) coiled coil protein [<i>Schizosaccharomyces pombe</i>] ; putative transporter C11D3.18C ; (Z68166) unknown [<i>Schizosaccharomyces pombe</i>] (AJ010262) MT5-MMP protein [<i>Mus musculus</i>]
17116	ENU00910	ANI61C7525: 48-67 8274..8659	452-479		EST	"z7c06a1.r1, z7c06a1.fl"		918	42	0.003			
17117	ENU00911	ANI61C1106 22-45 7:1012..1146	431-458		EST	"j4a04a1.r1, j4a04a1.fl"		536	33	1.6			
17118	ENU00912	ANI61C4849: 38-57 611..413	436-461		EST	"g0f03a1.r1, g0f03a1.fl"		754	57	0.000000 06			
17119	ENU00913	ANI61C7771: 26-47 4777..3187	787-814		EST	"g4e02a1.r1, g4e02a1.fl"		2308	37	0.21			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17120	ENU00914	ANI61C1042 9:2617..3123	22-42	455-474	EST	"w7h05a1.r1, w7h05a1.fl"		3172	32	2.7			hydroxyproline-rich glycoprotein - maize ; (X63134) hydroxyproline-rich glycoprotein [Zea mays] ; Hyp-rich glycoprotein [Zea mays]
17121	ENU00915	ANI61C2120: 1531..1896	78-101	454-479	EST	"r4e04a1.r1, r4e04a1.fl"		1204	41	0.004			hypothetical protein YDR514c - yeast (Saccharomyces cerevisiae) ; (U33057) Ydr514cp [Saccharomyces cerevisiae] ; (U33057) No definition line found [Saccharomyces cerevisiae]
17122	ENU00916	ANI61C3320: 5548..4259	44-63	767-786	EST	"w7g10a1.r1, w7g10a1.fl"		1162	32	4			"alpha-1D adrenergic receptor (alpha 1D-adrenoceptor) (alpha-1A adrenergic receptor) ; (S80044) alpha 1d-adrenergic receptor [mice, brain, Peptide, 562 aa] [Mus sp.] "
17123	ENU00917	ANI61C8010: 1..1664	22-46	804-827	EST	"a0e06a1.r1, a0e06a1.fl"		764	56	0.000000 4			hypothetical protein YLR019w - yeast (Saccharomyces cerevisiae) ; (Z73191) ORF YLR019w [Saccharomyces cerevisiae]
17124	ENU00918	ANI61C9711: 1514..259			EST	"g2c02a1.r1, g2c02a1.fl"		2428	143	1E-33			(AF080599) Medusa [Emericella nidulans]
17125	ENU00919	ANI61C2577: 1..976	23-42	802-829	EST	"n0f06a1.r1, n0f06a1.fl"		1614	102	2E-35			proteasome component C1 (macropain subunit C1) (proteinase YSCE subunit 1) (multicatalytic endopeptidase complex subunit C1) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain YC1 - yeast (Saccharomyces cerevisiae) ; (M55436) yeast proteasome subunit YC1 [Saccharomyces cerevisiae] ; (Z75270) ORF YOR362c [Saccharomyces cerevisiae]
17126	ENU00920	ANI61C8013: 1140..1	117-136	712-730	EST	"m7a01a1.r1, m7a01a1.fl"		2952	34	1.8			"malate oxidoreductase (NAD), mitochondrial 65 KD isoform precursor (malic enzyme) (ME) (NAD-dependent malic enzyme) (NAD-ME) ; malate dehydrogenase (decarboxylating) (EC 1.1.1.39) precursor, mitochondrial - prince's feather ; (U01162) C4 photosynthetic NAD-dependent malic enzyme subunit alpha precursor [Amaranthus hypochondriacus] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17127	ENU00921	ANI61C8963: 22-46 5134..4659		339-362	EST	"m8a06a1.r1, m8a06a1.fl"		1751	34	0.89			Centromere protein C (CENP-C) (centromere autoantigen C); centromere protein C - human; (M95724) centromere autoantigen C [Homo sapiens]
17128	ENU00922	ANI61C7935: 60-87 2554..2136		452-479	EST	"z1c07a1.r1, z1c07a1.fl"		2524	121	3E-27			(U75874) sconCp [Emericella nidulans]
17129	ENU00923	ANI61C2272: 43-66 1615..1		715-742	EST	"t2f05a1.r1, t2f05a1.fl"		1880	116	1E-25			Ribose-phosphate pyrophosphokinase 1 (phosphoribosyl pyrophosphate synthetase 1); ribose-phosphate pyrophosphokinase (EC 2.7.6.1) PRPS1 - yeast (Saccharomyces cerevisiae); (X70069) ribose-phosphate pyrophosphokinase [Saccharomyces cerevisiae]; (L04130) phosphoribosylpyrophosphate synthetase [Saccharomyces cerevisiae]; (X74151) orf11; homologous to human ribose-phosphate PP-kinase [Saccharomyces cerevisiae]; (Z28181) ORF YKL181w [Saccharomyces cerevisiae]
17130	ENU00924	ANI61C7364: 71-90 1423..2469		806-827	EST	"w7g01a1.r1, w7g01a1.fl"		1444	52	0.000006			(AC004697) unknown protein [Arabidopsis thaliana]
17131	ENU00925	ANI61C9397: 22-41 1765..1376		452-479	EST	"k0g08a1.r1, k0g08a1.fl"		746	31	7.8			(AF093543) transforming acidic coiled-coil containing protein 3 [Homo sapiens]
17132	ENU00926	ANI61C192:1 34-53 574..1		803-822	EST	"i8f03a1.r1, i8f03a1.fl"		985	51	0.00001			(Z98944) beta transducin [Schizosaccharomyces pombe]
17133	ENU00927	ANI61C1107 22-42 3:5748..4158		810-829	EST	"m2b12a1.r1, m2b12a1.fl"		2682	41	0.011			(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
17134	ENU00928	ANI61C1017 26-45 9:179..713		490-508	EST	"x7g07a1.r1, x7g07a1.fl"		1800	52	0.000002			hypothetical 63.5 KD protein ZK353.1 in chromosome III; ZK353.1 protein - Caenorhabditis elegans; (L15313) putative [Caenorhabditis elegans] (D00570) open reading frame (251 AA) [Mus musculus]
17135	ENU00929	ANI61C1048 37-56 4:6220..6375		457-479	EST	"w6d02a1.r1, w6d02a1.fl"		584	35	0.4			(AB011003) UDP-N-acetylglucosamine pyrophosphorylase [Candida albicans]
17136	ENU00930	ANI61C7526: 61-80 585..823		454-479	EST	"c9f03a1.r1, c9f03a1.fl"		960	100	1E-20			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
17137	ENU00931	ANI61C1132: 7881..8283			EST	"e9f09a1.r1, e9f09a1.fl"		1286	35	0.31			Immediate-early protein IE180 ; (X15120) immediate-early protein (AA 1-1460) [Pseudorabies virus]
17138	ENU00932	ANI61C1059 23-42 2:3950..4954	809-829		EST	"c5g03a1.r1, c5g03a1.fl"		1326	52	0.000006			CDC2+/CDC28-related protein kinase R2 ; protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice ; (X58194) cdc2+/CDC28-related protein kinase [Oryza sativa]
17139	ENU00933	ANI61C6527: 22-41 5800..6910	809-828		EST	"h1h05a1.r1, h1h05a1.fl"		1667	128	4E-29			(AJ001259) NIPSNAP2 protein [Homo sapiens]
17140	ENU00934	ANI61C7672: 34-53 4030..5198	807-829		EST	"m8b06a1.r1, m8b06a1.fl"		1514	76	3E-13			(AL024499) cDNA EST EMBL:C08541 comes from this gene; cDNA EST EMBL:C07241 comes from this gene [Caenorhabditis elegans]
17141	ENU00935	ANI61C2286: 31-50 1..736	685-712		EST	"c4a07a1.r1, c4a07a1.fl"		779	57	1E-11			SNF2 protein homolog YBR245c - yeast (Saccharomyces cerevisiae) (D14072) Homoserine kinase [Methylobacillus glycogenes]
17142	ENU00936	ANI61C1137 22-41 2:314..1056	658-682		EST	"s8a02a1.r1, s8a02a1.fl"		2469	32	3.4			(AF016419) contains similarity to the class II chitinases [Caenorhabditis elegans]
17143	ENU00937	ANI61C1140 34-56 4:3102..1439	805-829		EST	"r5a03a1.r1, r5a03a1.fl"		2678	39	0.031			
17144	ENU00938	ANI61C7672: 5304..5172			EST	"z4h12a1.r1, z4h12a1.fl"		478					"glyceraldehyde 3-phosphate dehydrogenase (GAPDH) ; glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - yeast (Zygosaccharomyces rouxii) ; (D00134) glyceraldehyde-3-phosphate dehydrogenase [Zygosaccharomyces rouxii] ; dehydrogenase, glyceraldehydephosphate [Zygosaccharomyces rouxii]"
17145	ENU00939	ANI61C1140 64-83 4:4368..3759	562-589		EST	"c5d10a1.r1, c5d10a1.fl"		2348	127	8E-29			(AC002387) putative reverse transcriptase [Arabidopsis thaliana] probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) ; (U20865) Yhr251 wp [Saccharomyces cerevisiae]
17146	ENU00940	ANI61C7366: 29-56 1228..778	448-475		EST	"t2g04a1.r1, t2g04a1.fl"		1578	34	0.69			
17147	ENU00941	ANI61C528:2 59-78 305..3935	788-807		EST	"s8c04a1.r1, s8c04a1.fl"		2977	37	0.21			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17148	ENU00942	ANI61C1140 4:499..1235	43-62	672-699	EST	"g2a10a1.r1, g2a10a1.fl"		1080	44	0.000000			Response regulator MCS4 (mitotic catastrophe suppressor 4) ; (Y11927) Msc4 protein [Schizosaccharomyces pombe] ; (AF004694) Msc4 [Schizosaccharomyces pombe] ; (AL033388) response regulator mcs4 [Schizosaccharomyces pombe] Amidophosphoribosyltransferase (glutamine phosphoribosylpyrophosphate amidotransferase) (ATase) ; (U32992) glutamine phosphoribosylpyrophosphate amidotransferase [Saccharomyces kluyveri] "high molecular mass early light-inducible protein precursor (ELIP) (clone HV58) ; early light-induced protein, high molecular weight, precursor (clone HV58) - barley chloroplast ; (X15693) precursor peptide (AA -31 to 200) [Hordeum vulgare] " phosphoribosylaminoimidazolecarboxamide formyltransferase 2 (aicar transformylase) / IMP cyclohydrolase (inosinase) (IMP synthetase) (ATIC) ; hypothetical protein YMR120c - yeast (Saccharomyces cerevisiae) ; (Z49273) unknown [Saccharomyces cerevisiae] Fibrillarin (nucleolar protein 1) ; nucleolar protein NOP1 - yeast (Saccharomyces cerevisiae) ; (J05230) fibrillarin [Saccharomyces cerevisiae] ; (Z48432) nucleolar protein NOP1 (J05230) [Saccharomyces cerevisiae] ; (Z74062) ORF YDL014w [Saccharomyces cerevisiae]
17149	ENU00943	ANI61C8832: 1..2242	30-49	805-829	EST	"r5c10a1.r1, r5c10a1.fl"		1177	136	6E-51			
17150	ENU00944	ANI61C2967: 2113..2695	22-48	459-485	EST	"z1g08a1.r1, z1g08a1.fl"		2132	36	0.22			
17151	ENU00945	ANI61C1049 5:2235..2509	30-49	456-479	EST	"t2g09a1.r1, t2g09a1.fl"		634	67	3E-24			
17152	ENU00946	ANI61C6247: 1430..2985	50-69	803-829	EST	"g6e01a1.r1, g6e01a1.fl"		1061	279	2E-74			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17153	ENU00947	ANI61C4858: 24-44 2982..1883	24-44	799-826	EST	"d5b09a1.r1, d5b09a1.fl"		2712	60	7E-13			3-oxoacyl-[acyl-carrier protein] reductase (3-ketoacyl-acyl carrier protein reductase) ; (Z99112) 3- ketoacyl-acyl carrier protein reductase [Bacillus subtilis] (Y14446) thylacine 1 [Xenopus laevis]
17154	ENU00948	ANI61C2136: 102-127 1..538	102-127	455-482	EST	"13b08a1.r1, 13b08a1.fl"		1258	31	5			probable succinyl-CoA:3-ketoacid- coenzyme A transferase precursor (3- oxoacid CoA-transferase) ; (Z48178) similar to 3-oxoacid CoA-transferase; cDNA EST EMBL:Z14816 comes from this gene; cDNA EST
17155	ENU00949	ANI61C465:7 33-51 090..7491	33-51	425-452	EST	"q0b02a1.r1, q0b02a1.fl"		1258	120	5E-27			probable succinyl-CoA:3-ketoacid- coenzyme A transferase precursor (3- oxoacid CoA-transferase) ; (Z48178) similar to 3-oxoacid CoA-transferase; cDNA EST EMBL:Z14816 comes from this gene; cDNA EST
17156	ENU00950	ANI61C3864: 1..297			EST	"t2f07a1.r1, t2f07a1.fl"		1146	29	7.5			EMBL:Z14946 comes from this gene; cDNA EST EMBL:D69746 comes from this gene; cDNA EST yk219b6.3 comes from this gene; cDNA EST y... (X06830) uracil permease (AA 1-633) [Saccharomyces cerevisiae]
17157	ENU00951	ANI61C4216: 22-48 362..635	22-48	440-467	EST	"c1f08a1.r1, c1f08a1.fl"		1018	33	1.2			(Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (L16844) yps-3 [Histoplasma capsulatum]
17158	ENU00952	ANI61C919:2 43-70 555..1951	43-70	562-584	EST	"i8h09a1.r1, i8h09a1.fl"		1074	146	2E-34			(AL022121) hypothetical protein Rv3677c [Mycobacterium tuberculosis]
17159	ENU00953	ANI61C1708: 204-223 3798..3145	204-223	590-609	EST	"k0e02a1.r1, k0e02a1.fl"		960	45	0.0004			immediate-early protein pip92 - mouse ; (M59821) growth factor-inducible protein [Mus musculus] ; (L26490) growth factor inducible immediate early protein [Mus musculus]
17160	ENU00954	ANI61C8676: 67-91 1123..1195	67-91	452-479	EST	"q0h01a1.r1, q0h01a1.fl"		232	32	3.5			3-isopropylmalate dehydrogenase (beta-IPM dehydrogenase) (IMDH) (3- IPM-DH) ; probable 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - Lactococcus lactis subsp. lactis ; (U92974) LeuB [Lactococcus lactis] (L42348) HOL1 [Saccharomyces cerevisiae]
17161	ENU00955	ANI61C1709: 51-70 2473..1562	51-70	806-829	EST	"i7g01a1.r1, i7g01a1.fl"		1540	31	9.1			
17162	ENU00956	ANI61C1311: 836..566			EST	"q0a06a1.r1, q0a06a1.fl"		894	39	0.005			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17163	ENU00957	ANI61C6704: 2767..2307	22-44	444-469	EST	"c6a05a1.r1, c6a05a1.fl"		1200	57	0.000000			"STE50 protein ; STE50 protein - yeast (Saccharomyces cerevisiae) ; (Z11116) STE50 protein [Saccharomyces cerevisiae] ; (X59720) YCL032w, len:346 [Saccharomyces cerevisiae] " (AL031350) putative secreted protein [Streptomyces coelicolor] (U34998) Rad9 [Coprinus cinereus]
17164	ENU00958	ANI61C1419: 713..267	23-46	455-478	EST	"d5e02a1.r1, d5e02a1.fl"		787	34	0.69			troponin:isotype=T [Oryctolagus cuniculus]
17165	ENU00959	ANI61C1099: 3348..2260			EST	"w7a08a1.r1, w7a08a1.fl"		1161	78	6E-14			(Z96072) hypothetical protein Rv2704 [Mycobacterium tuberculosis]
17166	ENU00960	ANI61C4365: 8..835	91-108	705-727	EST	"m8d07a1.r1, m8d07a1.fl"		1108	34	1.7			(AL049485) probable acetyl coA acetyltransferase (thiolase)
17167	ENU00961	ANI61C9733: 998..2932	27-46	774-798	EST	"m8h06a1.r1, m8h06a1.fl"		2491	54	0.000001			[Streptomyces coelicolor]
17168	ENU00962	ANI61C1141 0:1441..2506			EST	"t2e06a1.r1, t2e06a1.fl"		2520	32	4			(AC005314) dnaJ-like protein [Arabidopsis thaliana]
17169	ENU00963	ANI61C7677: 1..1476			EST	"i2f01a1.r1, i2f01a1.fl"		2444	36	0.35			hypothetical 27.9 KD protein in TRER-ACOA intergenic region ; (D83967) YfjR [Bacillus subtilis] ; (Z99108) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis] ; (D78509) YfjR [Bacillus subtilis]
17170	ENU00964	ANI61C3972: 3664..2542	33-50	809-829	EST	"e4a03a1.r1, e4a03a1.fl"		2818	76	3E-13			
17171	ENU00965	ANI61C7377: 774..693			EST	"c5b04a1.r1, c5b04a1.fl"		314					(AF000381) non-functional folate binding protein [Homo sapiens]
17172	ENU00966	ANI61C1253: 2367..2856	22-45	443-462	EST	"n3d08a1.r1, n3d08a1.fl"		1312	95	3E-19			(AB007867) KIAA0407 [Homo sapiens]
17173	ENU00967	ANI61C1253: 3473..4542	27-46	789-806	EST	"y6f01a1.r1, y6f01a1.fl"		1530	33	2.3			Folate receptor beta precursor (FR-beta) (folate receptor 2) (folate-binding protein 2) ; folate-binding protein 2 precursor - mouse ; (M64817) folate-binding protein 2 [Mus musculus]
17174	ENU00968	ANI61C1065 7:2436..4372	22-49	800-819	EST	"g5g02a1.r1, g5g02a1.fl"		1414	34	1.8			(AE001585) Polymorphic Outer Membrane Protein G Family [Chlamydia pneumoniae]
17175	ENU00969	ANI61C2979: 1..128			EST	"f0g10a1.r1, f0g10a1.fl"		508	29	4.8			(U90722) iron superoxide dismutase A [Trypanosoma cruzi]
17176	ENU00970	ANI61C8041: 1..2081	22-45	809-829	EST	"o8h08a1.r1, o8h08a1.fl"		2584	32	6.9			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
17177	ENU00971	ANI61C754:1 714..2949	32-51	789-809	EST	"w8e12a1.r1, w8e12a1.fl"		1788	216	1E-55			(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] chorion protein B11 [Bombyx mori]
17178	ENU00972	ANI61C7686: 376..186			EST	"w6gl2a1.r1, w6gl2a1.fl"		722	37	0.1			(D87071) similar to C.elegans protein encoded in cosmid T20D3 (Z68220). [Homo sapiens]
17179	ENU00973	ANI61C1253: 44-63 1736..2028	44-63	439-458	EST	"c4d11a1.r1, c4d11a1.fl"		900	32	2			probable membrane protein YLR409c - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr409cp [Saccharomyces cerevisiae]
17180	ENU00974	ANI61C9961: 22-42 3208..1496	22-42	805-829	EST	"o8e11a1.r1, o8e11a1.fl"		1770	93	3E-41			(AP000003) 323aa long hypothetical oligopeptide transport ATP-binding protein APPF [Pyrococcus horikoshii] PHO85 protein - yeast (Saccharomyces cerevisiae) ; (U43503) Lph16p [Saccharomyces cerevisiae]
17181	ENU00975	ANI61C538:5 50-72 861..4655	50-72	802-829	EST	"j7e12a1.r1, j7e12a1.fl"		1070	31	9.1			(AJ132944) G protein alpha subunit [Sclerotinia sclerotiorum]
17182	ENU00976	ANI61C8580: 22-40 10160..10494	22-40	456-475	EST	"t2e04a1.r1, t2e04a1.fl"		1244	45	0.0005			"iron(III) dicitrate transport protein fecB precursor, periplasmic - Escherichia coli ; (M26397) fecB [Escherichia coli]"
17183	ENU00977	ANI61C3642: 333..2055			EST	"x7h06a1.r1, x7h06a1.fl"		2534	64	3E-22			(U42580) a197R [Paramecium bursaria]
17184	ENU00978	ANI61C1253: 22-48 4323..4874	22-48	493-512	EST	"r8a05a1.r1, r8a05a1.fl"		799	32	3			Chlorella virus 1]
17185	ENU00979	ANI61C1044 39-66 5:2744..2913	39-66	446-472	EST	"g9g07a1.r1, g9g07a1.fl"		556	32	2			melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium] (Z98209) hypothetical protein Rv2735c [Mycobacterium tuberculosis]
17186	ENU00980	ANI61C4924: 36-63 2118..1286	36-63	791-812	EST	"g7e09a1.r1, g7e09a1.fl"		988	136	3E-31			(X94355) D17L [Cowpox virus] ; (Y11842) C17L [Cowpox virus] (AF000381) non-functional folate binding protein [Homo sapiens]
17187	ENU00981	ANI61C7851: 23-41 2891..347	23-41	785-804	EST	"h0g09a1.r1, h0g09a1.fl"		1996	34	1.4			
17188	ENU00982	ANI61C5537: 22-49 2750..1911	22-49	745-770	EST	"j7b07a1.r1, j7b07a1.fl"		1386	31	8.9			
17189	ENU00983	ANI61C1253: 54-75 2871..3085	54-75	414-433	EST	"w9b12a1.r1, w9b12a1.fl"		828	122	2E-27			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17190	ENU00984	ANI61C7436: 22-47 3010..3766	22-47	662-689	EST	"n0a07a1.r1, n0a07a1.fl"		2622	39	0.027			mitochondrial import receptor subunit TOM40 (MOM38 protein) (transLOC of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa] "Potassium transport protein, high-affinity ; potassium transport protein TRK1, high-affinity - yeast (Saccharomyces cerevisiae) ; (M21328) potassium transporter (put.) ; putative [Saccharomyces cerevisiae] ; (Z49404) ORF YJL129c [Saccharomyces cerevisiae] " probable peroxisomal membrane protein PMP20 (allergen ASP F 3) ; (U58050) peroxisomal-like protein [Aspergillus fumigatus] hypothetical 21.6 KD protein CY251.07 ; (Z74410) hypothetical protein Rv0089 [Mycobacterium tuberculosis] (AF006829) slow myosin heavy chain 2 [Coturnix coturnix]
17191	ENU00985	ANI61C3176: 22-46 767..1801	22-46	805-829	EST	"x9g10a1.r1, x9g10a1.fl"		1644	35	0.61			
17192	ENU00986	ANI61C5927: 51-71 398..139	51-71	417-443	EST	"o0h05a1.r1, o0h05a1.fl"		998	51	0.000006			
17193	ENU00987	ANI61C2449: 22-48 514..335	22-48	416-443	EST	"z1c10a1.r1, z1c10a1.fl"		666	41	0.005			
17194	ENU00988	ANI61C1019 0:1..252	22-48	176-196	EST	"m5e01a1.r1, m5e01a1.fl"		1000	29	5.3			
17195	ENU00989	ANI61C5024: 1..88			EST	"o0b12a1.r1, o0b12a1.fl"		348					
17196	ENU00990	ANI61C1021 7:1032..1784	22-46	705-732	EST	"d5h11a1.r1, d5h11a1.fl"		1270	39	0.046			(U19615) LET 858 [Caenorhabditis elegans] ; (Z81525) cDNA EST yk282b7.5 comes from this gene; cDNA EST EMBL:D28011 comes from this gene; cDNA EST EMBL:D28010 comes from this gene; cDNA EST EMBL:D33543 comes from this gene; cDNA EST EMBL:D36381 comes from this gene; cDNA ... glutamine synthetase (glutamate-- ammonia ligase) ; (L78067) glutamine synthetase [Glomerella cingulata]
17197	ENU00991	ANI61C1005: 23-42 351..885	23-42	420-444	EST	"l3c09a1.r1, l3c09a1.fl"		1536	130	6E-30			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
17198	ENU00992	ANI61C2206: 22-48 2704..3989		729-749	EST	"y8c08a1.r1, y8c08a1.fl"		2464	146	1E-34			putative nicotinate-nucleotide pyrophosphorylase (carboxylating) (quinolinate phosphoribosyltransferase (decarboxylating)) (QAPRTase) ; hypothetical protein YFR047c - yeast (Saccharomyces cerevisiae) ; (D50617) YFR047C [Saccharomyces cerevisiae] ; (D44597) unknown [Saccharomyces cerevisiae] (U60315) MC157R [Molluscum contagiosum virus subtype 1]
17199	ENU00993	ANI61C3359: 109-131 404..571		459-479	EST	"j0a12a1.r1, j0a12a1.fl"		626	31	4.6			
17200	ENU00994	ANI61C7960: 6227..6123			EST	"w9g10a1.r1, w9g10a1.fl"		378					
17201	ENU00995	ANI61C7447: 22-49 4468..4870		446-467	EST	"j9e03a1.r1, j9e03a1.fl"		1296	31	4.6			Envelope polyprotein GP160 precursor (contains: GP120 and GP41) ; (M29975) env polyprotein [Simian immunodeficiency virus]
17202	ENU00996	ANI61C1044 6:195..405		142-166 343-370	EST	"g2b12a1.r1, g2b12a1.fl"		768	123	4E-28			pyruvate decarboxylase ; (U73194) pyruvate decarboxylase [Emericella nidulans]
17203	ENU00997	ANI61C1650: 389..165			EST	"k0g02a1.r1, k0g02a1.fl"		858					PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]
17204	ENU00998	ANI61C4762: 55-74 1571..931		597-620	EST	"g3b05a1.r1, g3b05a1.fl"		1282					
17205	ENU00999	ANI61C379:3 906..5711		763-790	EST	"g5a12a1.r1, g5a12a1.fl"		2452	41	0.011			
17206	ENU01000	ANI61C1160: 22-45 9772..7996		807-829	EST	"m2e11a1.r1, m2e11a1.fl"		3110					
17207	ENU01001	ANI61C8118: 23-43 1281..1515		454-479	EST	"o8g10a1.r1, o8g10a1.fl"		898	32	3.5			hypothetical 52.0 KD protein in RPL17A-BOB1 intergenic region ; hypothetical protein YBL086c - yeast (Saccharomyces cerevisiae) ; (X79489) D-466 protein [Saccharomyces cerevisiae] ; (Z35847) ORF YBL086c [Saccharomyces cerevisiae]
17208	ENU01002	ANI61C4702: 37-56 988..662		453-479	EST	"q0b06a1.r1, q0b06a1.fl"		1112					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17209	ENU01003	ANI61C9802: 3344..2176	67-86	799-826	EST	"w6b07a1.rl, w6b07a1.fl"		1844	115	4E-25			hypothetical 62.4 KD protein in GLS1-KAP95 intergenic region precursor ; probable membrane protein YLR343w - yeast (Saccharomyces cerevisiae) ; (U19028) Ylr343wp [Saccharomyces cerevisiae]
17210	ENU01004	ANI61C8507: 22-45 2551..504	22-45	805-829	EST	"y8a02a1.rl, y8a02a1.fl"		2922	36	0.35			(AF038388) actin-filament binding protein Frabin [Rattus norvegicus] (AB017627) acetyltransferase [Candida albicans]
17211	ENU01005	ANI61C1110 22-47 9:1779..969	22-47	747-774	EST	"c9g10a1.rl, c9g10a1.fl"		1110	108	2E-28			"40S ribosomal protein S30 ; ribosomal protein S30.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (U48699) Rps30ap [Saccharomyces cerevisiae] ; (U48700) ytpS30 [Saccharomyces cerevisiae] ; (U17243) L8003.23 gene product [Saccharomyces cerevisiae] ; (Z75090) ORF YOR182c [Saccharomyces cerevisiae] ; (U83406) Rps30bp [Saccharomyces cerevisiae] ; (U83407) Rps30bp [Saccharomyces cerevisiae]"
17212	ENU01006	ANI61C1110 57-76 9:67..636	57-76	522-549	EST	"d5d04a1.rl, d5d04a1.fl"		1892	51	0.000007			Sodium/hydrogen exchanger 4 (NA(+)/H(+) exchanger 4) (NHE-4) ; Na+/H+-exchanging protein 4 - rat ; (M85301) sodium-hydrogen exchange protein-isoform 4 [Rattus norvegicus]
17213	ENU01007	ANI61C5934: 115-133 26..419	115-133	376-398	EST	"c7d03a1.rl, c7d03a1.fl"		1473	33	1.2			(AB010442) PMR1 [Penicillium digitatum]
17214	ENU01008	ANI61C2384: 22-47 1274..2113	22-47	792-819	EST	"j7d01a1.rl, j7d01a1.fl"		1128					"Insulin-like growth factor binding protein 2 precursor (IGFBP-2) (IBP-2) (IGF-binding protein 2) ; insulin-like growth factor-binding protein-2 - sheep ; (S44612) insulin-like growth factor-binding protein-2, IGFBP-2 [sheep, Peptide, 317 aa] [Ovis aries]"
17215	ENU01009	ANI61C9175: 22-42 2292..4912	22-42	798-825	EST	"q0g01a1.rl, q0g01a1.fl"		1669	254	6E-88			(M19113) env polyprotein [Rous-associated virus type 1]
17216	ENU01010	ANI61C8913: 22-47 2865..2634	22-47	434-457	EST	"r4b02a1.rl, r4b02a1.fl"		912	31	6			
17217	ENU01011	ANI61C1052 44-67 7:620..1	44-67	500-519	EST	"r1a07a1.rl, r1a07a1.fl"		1744	32	2.7			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17218	ENU01012	ANI61C8273: 5678..6704	38-57	785-812	EST	"g4c02a1.r1, g4c02a1.fl"		2766	234	7E-61			"mitochondrial 60S ribosomal protein L9 precursor (YML9) ; ribosomal protein L3 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X87941) ORF 269 [Saccharomyces cerevisiae] ; (Z73004) ORF YGR220c [Saccharomyces cerevisiae] "
17219	ENU01013	ANI61C2166: 1988..875	24-47	762-785	EST	"m0h08a1.r1, m0h08a1.fl"		1984	164	4E-51			"peptide transporter PTR2-A ; (U01171) similar to S. cerevisiae PTR2 gene, GenBank Accession Number L11994 [Arabidopsis thaliana] "
17220	ENU01014	ANI61C7324: 1345..1	22-47	772-792	EST	"s8h02a1.r1, s8h02a1.fl"		1576					(AB008791) Phosphoinositide 3-Kinase-C2gamma [Mus musculus]
17221	ENU01015	ANI61C4383: 1070..1715	22-45	587-614	EST	"x9f09a1.r1, x9f09a1.fl"		1518					TTP1 protein ; TTP1 protein - yeast (Saccharomyces cerevisiae) ; (Z35884) ORF YBR015c [Saccharomyces cerevisiae]
17222	ENU01016	ANI61C4007: 126..2015	29-48	802-829	EST	"g7a12a1.r1, g7a12a1.fl"		1528	32	6.9			
17223	ENU01017	ANI61C9760: 5294..4181	44-63	807-829	EST	"c5a08a1.r1, c5a08a1.fl"		1588	81	9E-15			
17224	ENU01018	ANI61C4167: 1081..1	22-45	719-746	EST	"f2f09a1.r1, f2f09a1.fl"		3198					(AE001093) A. fulgidus predicted coding region AF0189 [Archaeoglobus fulgidus]
17225	ENU01019	ANI61C1178: 975..1	22-41	730-749	EST	"g4h05a1.r1, g4h05a1.fl"		1580	34	1.4			hypothetical 42.0 KD protein in thi12-RPD3 intergenic region ; probable aryl-alcohol dehydrogenase YNL331c - yeast (Saccharomyces cerevisiae) ; (X83226) homologous to aryl-alcohol dehydrogenase of P.chrysosporium [Saccharomyces cerevisiae] ; (Z71607) ORF YNL331c [Saccharomyces cerevisiae]
17226	ENU01020	ANI61C5675: 3316..1999	22-48	799-826	EST	"m5a07a1.r1, m5a07a1.fl"		1486	288	3E-77			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17227	ENU01021	ANI61C4093: 441..92	47-66	456-478	EST	"o8h05a1.rl, o8h05a1.fl"		1380	49	0.00002			"acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 KD subunit) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 12K chain precursor - Neurospora crassa ; (X59258) NADH dehydrogenase (ubiquinone) 12 kD subunit [Neurospora crassa] ; (X83578) mitochondrial acyl carrier protein [Neurospora crassa] "
17228	ENU01022	ANI61C5291: 1953..703	22-46	805-829	EST	"j7g12a1.rl, j7g12a1.fl"		2592	80	2E-14			(Z99113) similar to alcohol dehydrogenase [Bacillus subtilis] ; (Z99114) similar to alcohol dehydrogenase [Bacillus subtilis]
17229	ENU01023	ANI61C6729: 1961..1860			EST	"c1e09a1.rl, c1e09a1.fl"		564					
17230	ENU01024	ANI61C1024 4:5995..6792	24-43	741-768	EST	"c9h08a1.rl, c9h08a1.fl"		1782	68	1E-10			Nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nirA - Emericella nidulans ; (M68900) NIRA protein [Emericella nidulans]
17231	ENU01025	ANI61C1045 2:2704..3893	59-78	800-827	EST	"flg10a1.rl, flg10a1.fl"		1146	71	1E-11			Pentafunctional arom polypeptide [contains: 3-dehydroquinase synthase ; 3-dehydroquinase dehydratase (3-dehydroquinase); shikimate 5-dehydrogenase ; shikimate kinase ; EPSP synthase] ; ARO1 protein - yeast (Saccharomyces cerevisiae) ; (X06077) arom multifunctional enzyme (AA 1-1588) [Saccharomyces cerevisiae] ; (Z48179) Aro 1p [Saccharomyces cerevisiae]
17232	ENU01026	ANI61C9977: 1302..3160	30-49	805-829	EST	"b0b05a1.rl, b0b05a1.fl"		1338	33	2.3			possible regulatory function (alternatively spliced) protein p30 II - Human T-cell leukemia virus type I (U83323) major surface glycoprotein [Pneumocystis carinii]
17233	ENU01027	ANI61C1052 7:3506..3746	44-63	458-479	EST	"t2g10a1.rl, t2g10a1.fl"		688	32	2.7			(U13672) beta-glucosidase [Candida wickerhamii] ; beta-glucosidase [Candida wickerhamii]
17234	ENU01028	ANI61C1052 9:7316..6486			EST	"t2h09a1.rl, t2h09a1.fl"		1505	182	1E-52			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17235	ENU01029	ANI61C6022: 1666..938	50-77	681-708	EST	"y8g05a1.r1, y8g05a1.fl"		1439	221	7E-59			(AB010442) PMR1 [Penicillium digitatum]
17236	ENU01030	ANI61C5297: 22-41	22-41	443-470	EST	"m0c08a1.r1, m0c08a1.fl"		566	31	6			(X85135) alpha-51D-immobilization antigen [Paramecium tetraurelia] (AE001617) Phopholipase D Superfamily [Chlamydia pneumoniae]
17237	ENU01031	ANI61C7000: 1379..1534	40-59	786-806	EST	"w8c11a1.r1, w8c11a1.fl"		745	34	1.3			"kynureninase (EC 3.7.1.3) - rat ; kynureninase, L-kynurenine hydrolase {EC 3.7.1.3} [rats, liver cytosol, Peptide, 464 aa] "
17238	ENU01032	ANI61C9509: 22-46	22-46	646-673	EST	"z3a08a1.r1, z3a08a1.fl"		1114	106	1E-23			
17239	ENU01033	ANI61C2073: 22-41	22-41	805-829	EST	"z3e11a1.r1, z3e11a1.fl"		1196					
17240	ENU01034	1786..656				"y8h10a1.r1, y8h10a1.fl"		1346	287	6E-77			"ATP synthase beta chain, mitochondrial precursor ; H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Neurospora crassa ; (X53720) F(1)-ATPase beta-subunit precursor (519 AA) [Neurospora crassa] ; (M84192) mitochondrial ATPase beta-subunit [Neurospora crassa] "
17241	ENU01035	ANI61C818:5 2..2394	60-79	780-799	EST	"d3e03a1.r1, d3e03a1.fl"		1482	31	9.1			"(AE001140) glu-tRNA amidotransferase, subunit B (gatB) [Borrelia burgdorferi] "
17242	ENU01036	ANI61C499:2 29..5	104-129	386-413	EST	"y6f12a1.r1, y6f12a1.fl"		853	32	2			[X64795] fatty-acid synthase [Corynebacterium ammoniagenes]
17243	ENU01037	ANI61C4773: 529..38	156-175	458-478	EST	"y6g08a1.r1, y6g08a1.fl"		1443	34	0.9			RCC1-like G exchanging factor RLG ; (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens]
17244	ENU01038	ANI61C412:5 479..3114	51-70	802-829	EST	"j0a03a1.r1, j0a03a1.fl"		1680	74	1E-12			hypothetical 83.0 KD protein in ATP1-ROX3 intergenic region ; hypothetical protein YBL097w - yeast (Saccharomyces cerevisiae) ; (X79489) C-728 protein [Saccharomyces cerevisiae] ; (Z35858) ORF YBL097w [Saccharomyces cerevisiae] (Z83866) hypothetical protein Rv3058c [Mycobacterium tuberculosis]
17245	ENU01039	ANI61C4395: 1..731	121-140	662-689	EST	"j0d06a1.r1, j0d06a1.fl"		1972	31	7.6			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17246	ENU01040	ANI61C317:4 22-43 271..5538		743-762	EST	"i2c04a1.rl, i2c04a1.fl"		1924	35	0.61			"glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAigsl1) - Arabidopsis thaliana ; (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] ; Gln synthetase [Arabidopsis thaliana]"
17247	ENU01041	ANI61C1070 22-40 2:2736..506		805-829	EST	"j9g11a1.rl, j9g11a1.fl"		2058	32	5.3			(U42580) a197R [Paramecium bursaria Chlorella virus 1]
17248	ENU01042	ANI61C9348: 1052..1165			EST	"y6f02a1.rl, y6f02a1.fl"		406	36	0.23			(AF081803) non-receptor protein tyrosine kinase laloo [Xenopus laevis]
17249	ENU01043	ANI61C7287: 35-54 411..698		456-479	EST	"p0a05a1.rl, p0a05a1.fl"		1740	138	5E-35			(AL031174) t-complex protein 1 gamma subunit homolog [Schizosaccharomyces pombe]
17250	ENU01044	ANI61C9662: 22-45 1428..3521		806-829	EST	"n8d02a1.rl, n8d02a1.fl"		3596	161	7E-42			(Z98598) putative transcriptional regulator [Schizosaccharomyces pombe]
17251	ENU01045	ANI61C9112: 25-48 5158..6271		800-827	EST	"j0h04a1.rl, j0h04a1.fl"		1162	31	9.1			"78 kDa apamin binding protein [cattle, brain synaptosomes, Peptide, 438 aa]"
17252	ENU01046	ANI61C1038 27-54 1:1514..1070		452-479	EST	"c5e06a1.rl, c5e06a1.fl"		1022	76	2E-13			(AE000776) molybdopterin converting factor subunit 2 [Aquifex aeolicus]
17253	ENU01047	ANI61C8620: 46-65 2890..1835		803-829	EST	"d5e10a1.rl, d5e10a1.fl"		2544	180	1E-44			Replication factor-A protein 1 (single-stranded DNA-binding protein P68 subunit) ; (U59385) single-stranded DNA binding protein p68 subunit [Schizosaccharomyces pombe] ; (U75446) Rpa1 [Schizosaccharomyces pombe] ; (AL034563) replication factor-a protein 1
17254	ENU01048	ANI61C1030 22-49 2:4028..5287		765-792	EST	"r2h07a1.rl, r2h07a1.fl"		2484	39	0.054			[Schizosaccharomyces pombe] mucin (clone PGM-2A) - pig ; gastric mucin - pig (fragment) ; (U10281)
17255	ENU01049	ANI61C1204: 46-73 906..1459		500-527	EST	"e0h10a1.rl, e0h10a1.fl"		1344	32	2.3			gastric mucin [Sus scrofa] maturase-related protein - maize (fragment) ; (U09987) maturase-related protein [Zea mays]
17256	ENU01050	ANI61C6602: 3140..3042			EST	"m0e08a1.rl, m0e08a1.fl"		362					
17257	ENU01051	ANI61C1046 22-44 2:3354..41		769-788	EST	"z4h03a1.rl, z4h03a1.fl"		4624	31	9.1			(U96487) V-ATPase proteolipid [Desulfurococcus sp. SY]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17258	ENU01052	ANI61C8867: 271..1			EST	"w6f07a1.r1, w6f07a1.fl"		646	42	0.000000			hypothetical oxidoreductase in KGD1-SIM1 intergenic region ; probable membrane protein YIL124w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae] (Y17554) ornithine carbamoyltransferase [Bacillus licheniformis] (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
17259	ENU01053	ANI61C8772: 66-85 1349..1162		454-479	EST	"g3a06a1.r1, g3a06a1.fl"		706	31	4.6			
17260	ENU01054	ANI61C1071 40-60 3:1384..3265		802-829	EST	"g2f07a1.r1, g2f07a1.fl"		1135	33	2.3			
17261	ENU01055	ANI61C4672: 22-49 798..1		711-738	EST	"v7d01a1.r1, v7d01a1.fl"		3663	70	2E-11			Defender against cell death 1 (DAD-1) ; (D86562) DAD1 protein [Sus scrofa] (AB001488) similar to ORF14 of <i>enterococcus faecalis</i> transposon TN916. [Bacillus subtilis] ; (Z99106) similar to transposon protein [Bacillus subtilis]
17262	ENU01056	ANI61C7906: 58-85 1632..963		623-646	EST	"d4a06a1.r1, d4a06a1.fl"		1202	33	2.3			hypothetical protein 1 - Porphyromonas gingivalis ; transposase [Porphyromonas gingivalis]
17263	ENU01057	ANI61C6993: 29-48 1951..2151		442-461	EST	"d2h03a1.r1, d2h03a1.fl"		562	32	2.7			
17264	ENU01058	ANI61C2402: 38-57 2788..1770		802-829	EST	"m0d10a1.r1, m0d10a1.fl"		1676					
17265	ENU01059	ANI61C6033: 49-76 836..1		735-762	EST	"r5g05a1.r1, r5g05a1.fl"		4528	47	0.0002			(AF026977) microsomal glutathione S-transferase 3 [Homo sapiens]
17266	ENU01060	ANI61C1113 22-49 0:5863..5477		442-469	EST	"r2d04a1.r1, r2d04a1.fl"		1365	33	1.2			(Z49806) adenylyl cyclase type VII [Bos taurus]
17267	ENU01061	ANI61C1113 25-45 0:6242..7566		802-829	EST	"g6h02a1.r1, g6h02a1.fl"		1386	32	5.3			(Y00318) heavy chain of factor I [Homo sapiens]
17268	ENU01062	ANI61S4418: 48-74 263..437		392-416	EST	"p0f02a1.r1, p0f02a1.fl"		474					
17269	ENU01063	ANI61C710:9 53-72 84..892		406-433	EST	"z4a06a1.r1, z4a06a1.fl"		316	31	7.8			B-lymphocyte antigen CD19 precursor - mouse ; (M62542) CD19 [Mus musculus]
17270	ENU01064	ANI61C4270: 22-41 2290..3972		792-819	EST	"i3g06a1.r1, i3g06a1.fl"		1208	46	0.0004			(Z98979) tat binding homolog [Schizosaccharomyces pombe]
17271	ENU01065	ANI61C7744: 49-68 2557..2444		444-466	EST	"i0c09a1.r1, i0c09a1.fl"		402	64	2E-19			methionyl aminopeptidase (EC 3.4.11.18) 2 - rat ; (L10652) initiation factor 2 associated 67 kDa protein [Rattus rattus]

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17272	ENU01066	ANI61C1765: 22-45 2877..1842		802-829	EST	"h1a09a1.r1, h1a09a1.fl"		1438	148	6E-40			hypothetical 27.4 KD protein in MER2-BNA1 intergenic region ; hypothetical protein YJR024c - yeast (Saccharomyces cerevisiae) ; (Z49524) ORF YJR024c [Saccharomyces cerevisiae] ; (X87297) J1545 [Saccharomyces cerevisiae] (AF003136) F28B3.6 [Caenorhabditis elegans] homoserine O-acetyltransferase (homoserine O-trans-acetylase) ; homoserine O-acetyltransferase (EC 2.3.1.31) - fungus (Ascobolus immersus) ; (M26662) met2 [Ascobolus immersus] probable sucrose utilization protein SUC1 transcription factor XLFB1a - African clawed frog (AF109904) type IV-A pilus assembly protein PilC [Vibrio cholerae] Insulin-degrading enzyme (insulysin) (insulinase) (insulin protease) ; (M21188) insulin-degrading enzyme [Homo sapiens] "unknown ; (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens] " hypothetical 69.5 KD protein C22G7.05 in chromosome I ; hypothetical protein SPAC22G7.05 - fission yeast (Schizosaccharomyces pombe) ; (Z54328) hypothetical protein [Schizosaccharomyces pombe] (Z83860) hypothetical protein Rv2337c [Mycobacterium tuberculosis] PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]
17273	ENU01067	ANI61C1768: 106-125 2263..1583		636-660	EST	"p0f03a1.r1, p0f03a1.fl"		3281	33	1.8			
17274	ENU01068	ANI61C1144 35-53 6:1583..803		724-743	EST	"i7e07a1.r1, i7e07a1.fl"		1538	141	5E-33			
17275	ENU01069	ANI61C4601: 34-53 1044..2517		801-820	EST	"g9h06a1.r1, g9h06a1.fl"		1910	66	4E-10			
17276	ENU01070	ANI61C8638: 22-47 1299..208		802-821	EST	"i8b01a1.r1, i8b01a1.fl"		822	37	0.21			
17277	ENU01071	ANI61C1999: 22-48 284..176		341-368	EST	"c1d12a1.r1, c1d12a1.fl"		360	32	2.5			
17278	ENU01072	ANI61C1190: 43-63 9336..7397		804-829	EST	"j0g08a1.r1, j0g08a1.fl"		1287	85	5E-16			
17279	ENU01073	ANI61C1496: 692..1			EST	"j4d05a1.r1, j4d05a1.fl"		1035	45	0.0006			
17280	ENU01074	ANI61C7238: 30-56 1608..3544		767-794	EST	"l3c11a1.r1, l3c11a1.fl"		1462	101	7E-21			
17281	ENU01075	ANI61C6857: 23-46 2312..1825		451-472	EST	"c5f05a1.r1, c5f05a1.fl"		1376	31	4.6			
17282	ENU01076	ANI61C8941: 55-82 446..1359		806-829	EST	"j7b09a1.r1, j7b09a1.fl"		1136	41	0.011			

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17283	ENU01077	ANI61C1056: 1179..950	31-49	345-372	EST	"o8a03a1.rl, o8a03a1.fl"		858	30	7.8			(AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL:D75425 comes from this gene; cDNA EST EMBL:M89392 comes from this gene; cDNA EST EMBL:M89303 comes from this gene; cDNA EST EMBL:D27766 comes from this gene; cDNA EST ... (AL023290) putative serine-rich zinc-finger protein [Schizosaccharomyces pombe] (Z72496) mucin MUC5B [Homo sapiens] transPOSase ; (L49438) transposase [Chelatobacter heintzii] (AF051344) latent transforming growth factor-beta binding protein 4S [Homo sapiens] LDL receptor 2 precursor - African clawed frog pyruvate kinase (PK) ; pyruvate kinase (EC 2.7.1.40) - Emericella nidulans ; (M36918) pyruvate kinase [Emericella nidulans] (Z92771) rmlA2 [Mycobacterium tuberculosis] (AL032647) predicted using Genefinder [Caenorhabditis elegans] (AF057557) anti-Fas-induced apoptosis [Homo sapiens] (AF088906) clock-controlled gene-9 protein [Neurospora crassa] (U76621) short-chain alcohol dehydrogenase [Aspergillus parasiticus]
17284	ENU01078	ANI61C1191: 5322..4443	24-46	804-823	EST	"z7d04a1.rl, z7d04a1.fl"		1274	64	0.000000			
17285	ENU01079	ANI61C6579: 990..22	39-58	740-761	EST	"c5d09a1.rl, c5d09a1.fl"		2024	37	0.21			
17286	ENU01080	ANI61C3388: 1847..1622	22-49	457-477	EST	"y3c11a1.rl, y3c11a1.fl"		807	34	0.9			
17287	ENU01081	ANI61C7193: 2856..1594	22-46	757-784	EST	"g5e11a1.rl, g5e11a1.fl"		1572	32	5.3			
17288	ENU01082	ANI61C433:1 027..1492	45-72	425-452	EST	"c0f09a1.rl, c0f09a1.fl"		2400	38	0.061			
17289	ENU01083	ANI61C7805: 1604..1117	51-70	449-476	EST	"z3e12a1.rl, z3e12a1.fl"		1132	86	1E-27			
17290	ENU01084	ANI61C7912: 647..2376	37-56	802-829	EST	"d3g06a1.rl, d3g06a1.fl"		1350	32	5.3			
17291	ENU01085	ANI61C7016: 5055..5615	22-48	511-538	EST	"g3a07a1.rl, g3a07a1.fl"		3050	32	4.1			
17292	ENU01086	ANI61C9830: 5230..4032	22-41	783-802	EST	"r6g04a1.rl, r6g04a1.fl"		1709	34	1.4			
17293	ENU01087	ANI61C8362: 1533..741	22-49	738-765	EST	"w6e06a1.rl, w6e06a1.fl"		2643	36	0.43			
17294	ENU01088	ANI61C9371: 1572..223	22-42	794-821	EST	"y4f11a1.rl, y4f11a1.fl"		2612	51	0.000009			
17295	ENU01089	ANI61S420:4 5..458	47-68	391-418	TPEST								
17296	ENU01090	ANI61C5867: 916..1310	69-88	402-421	TPEST				32	1.9			(AL032684) ER lumen protein retaining receptor protein [Schizosaccharomyces pombe]

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17297	ENU01091	ANI61C1970: 85..504	22-47	382-399	TPEST								(AE001270) DNA helicase II (uvrD) [Treponema pallidum]
17298	ENU01092	ANI61C2877: 761..329	39-58	410-429	TPEST			32	32	2.1			(AE001556) putative [Helicobacter pylori J99]
17299	ENU01093	ANI61C9950: 1693..1253	31-50	410-429	TPEST			31	31	4.9			3-hydroxyisobutyrate dehydrogenase precursor (HIBADH) ; 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - rat (fragment) ; (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus norvegicus] (AL031004) putative protein [Arabidopsis thaliana]
17300	ENU01094	ANI61C6837: 2183..2659	22-44	437-456	TPEST			90	90	8E-18			
17301	ENU01095	ANI50C1_24 3:387..875	72-91	496-518	TPEST			31	31	7.6			
17302	ENU01096	ANI61C878:1 184..1678	38-60	469-490	TPEST								
17303	ENU01097	ANI61C7544: 771..1304	47-66	521-538	TPEST								
17304	ENU01098	ANI61C5207: 566..931	62-80	366-385	TPEST			30	30	6.3			(AC003952) hypothetical protein [Arabidopsis thaliana] ; (AC006201) hypothetical protein [Arabidopsis thaliana]
17305	ENU01099	ANI61C8333: 1221..1614	22-51	350-374	TPEST			62	62	0.000000			(U95045) velvet A [Emmericella nidulans]
17306	ENU01100	ANI61C3918: 2719..2318	31-55	371-390	TPEST			30	30	9.7			(AF007101) PKS module 2 [Streptomyces hygroscopicus]
17307	ENU01101	ANI61C9642: 1261..1663	22-51	356-382	TPEST			33	33	0.85			Choriongonadotropic hormone-like receptor (CGH-R) ; chorionic gonadotropin receptor - Xanthomonas maltophilia (fragment) ; (X68371) chorionic gonadotropin receptor homologue [Stenotrophomonas maltophilia]
17308	ENU01102	ANI50C9535 _1:677..1088	72-91	406-441	TPEST			30	30	7.7			"surface antigen 51A - Paramecium tetraurelia (SGC5) (fragments) ; protein 51A,surface [Paramecium tetraurelia] "
17309	ENU01103	ANI61C7666: 510..99	56-81	405-425	TPEST								
17310	ENU01104	ANI61C6789: 2590..3012	59-78	419-439	TPEST			31	31	3.5			"(X80835) len: 676, CAI: 0.13 [Saccharomyces cerevisiae] "

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17311	ENU01105	ANI61C4663:	22-41	391-410	TPEST				31	61	4.8	0.000000		(AE001440) Pantoate--beta-alanine ligase [Helicobacter pylori J99]
17312	ENU01106	ANI61C3646:	44-63	413-434	TPEST				61	61	0.000000	003		(Y13759) alpha-L-arabinofuranosidase [Emericella nidulans]
17313	ENU01107	ANI61C1044	55-74	430-449	TPEST				32	32	2.8	2.8		3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type IV (3beta-HSD IV) (3-beta-hydroxy-delta(5)-steroid dehydrogenase (3-beta-hydroxy-5-ENE steroid dehydrogenase) (progesterone reductase) / steroid delta-isoMERAS... ; 3beta-hydroxysteroid-Delta5-steroid dehydrogenase multifunctional protein IV - rat ; (L17138) 3 hydroxysteroid dehydrogenase [Rattus norvegicus] (AB007770) translation elongation factor 1 alpha [Aspergillus oryzae] (AL035524) pectinesterase like protein [Arabidopsis thaliana] (Z54236) similar to fibronectin type-III repeats; cDNA EST EMBL:D32588 comes from this gene; cDNA EST EMBL:D33928 comes from this gene; cDNA EST EMBL:D35265 comes from this gene; cDNA EST EMBL:D36890 comes from this gene; cDNA ...
17314	ENU01108	ANI61C1794:	34-53	421-442	TPEST				76	76	2E-13			
17315	ENU01109	ANI61C7967:	22-46	412-432	TPEST				34	34	0.45			
17316	ENU01110	ANI61C3092:	25-56	418-437	TPEST				33	33	1.3			

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17317	ENU01111	ANI61C8828: 22-46 1150..1606	22-46	413-436	TPEST				94	5E-19			phosphoribosyl pyrophosphate synthetase 1 ; ribose-phosphate pyrophosphokinase I (phosphoribosyl pyrophosphate synthetase I) (PRIBP) (PRS-I) ; ribose-phosphate pyrophosphokinase (EC 2.7.6.1) catalytic chain I - human ; ribose-phosphate pyrophosphokinase (EC 2.7.6.1) catalytic chain I - rat ; (X15331)
													phosphoribosylpyrophosphate synthetase (AA 1-319) [Homo sapiens] ; (X16554) ribose-phosphate pyrophosphokinase subunit I (AA 1-318) [Rattus norvegicus] ; (M31084)
													phosphoribosylpyrophosphate synthetase [Rattus norvegicus] ; (M29392)
													phosphoribosylpyrophosphate synthetase (PRPS1) precursor [Rattus norvegicus] ; (M17258) phosphoribosyl pyrophosphate synthetase I [Rattus norvegicus] ; (D00860) phosphoribosyl pyrophosphate synthetase subunit I [Homo sapiens]
17318	ENU01112	ANI61C201:2 23-58 02..135	23-58	415-438	TPEST				31	4			Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease ; reverse transcriptase ; endonuclease] ; hypothetical protein - common tobacco ; (X13777) ORF [Nicotiana tabacum]
17319	ENU01113	ANI61C8982: 22-52 6933..7395	22-52	423-442	TPEST								
17320	ENU01114	ANI61C1131 65-89 7:1154..1621	65-89	465-490	TPEST				41	0.004			probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) ; (Z48758) unknown [Saccharomyces cerevisiae]
17321	ENU01115	ANI61C5275: 43-65 515..41	43-65	454-475	TPEST								(AB023216) KIAA0999 protein [Homo sapiens]
17322	ENU01116	ANI61C562:7 44-63 984..7507	44-63	460-479	TPEST				33	1.1			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17323	ENU01117	ANI61C1758: 22-47	433-461	TPEST				42	0.003				(AL034433) hypothetical protein [Schizosaccharomyces pombe]
17324	ENU01118	ANI61C5576: 25-45	446-466	TPEST				33	1.5				hypothetical 69.0 KD protein in SIR1 3'region ; hypothetical protein YCL070C homolog YKR106w - yeast (Saccharomyces cerevisiae) ; (Z28202) ORF YKR106w [Saccharomyces cerevisiae]
17325	ENU01119	ANI61C9263: 28-49	459-479	TPEST				33	1.2				(AB013161) NADH dehydrogenase subunit 5 [Pieris rapae]
17326	ENU01120	ANI61C1516: 25-54	450-479	TPEST				37	0.11				(Z94043) hypothetical protein [Bacillus subtilis] ; (Z99121) similar to reticuline oxidase [Bacillus subtilis]
17327	ENU01121	ANI61C6698: 54-76	498-533	TPEST				152	9E-41				"(AB018078) oligo-1,4 - 1,4-glucantransferase / amylo-1,6-glucosidase [Saccharomyces cerevisiae] "
17328	ENU01122	ANI61C5920: 37-56	492-527	TPEST				32	3.9				"(Y15197) microtubule-associated protein, MAP-115 [Mus musculus] "
17329	ENU01123	ANI61C151:1 29-63	505-524	TPEST				103	1E-30				"ATP synthase subunit 4, mitochondrial precursor ; (AF019222) F1Fo-ATP synthase subunit 4 [Kluyveromyces lactis] "
17330	ENU01124	ANI61C6008: 39-60	546-580	TPEST				29	9.9				nucleic acid-binding protein E5.1 - human ; (L37368) RNA-binding protein [Homo sapiens]
17331	ENU01125	ANI61C9308: 51-70	338-357	TPEST				30	6.5				(AE000839) conserved protein [Methanobacterium thermoautotrophicum]
17332	ENU01126	ANI61C5797: 25-44	335-354	TPEST									

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17333	ENU01127	ANI61C5908: 49-68 1378..971	49-68	395-414	TPEST			208	1E-53			"5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (methionine synthase, vitamin-B12 independent isozyme) (cobalamin-independent methionine synthase) (delta-P8 protein) ; 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - yeast (Saccharomyces cerevisiae) ; (U18839) Met6p: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Saccharomyces cerevisiae] ; (U32508) N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae] " (AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea] ubiquitin - Mediterranean fruit fly ; ubiquitin [Homo sapiens] ; ubiquitin [Homo sapiens] ; ubiquitin [Scombridae gen. sp.] ; ubiquitin [Thunnus sp.] ribonucleoprotein - Arabidopsis thaliana ; (M98340) ribonucleoprotein [Arabidopsis thaliana] ; Ser/Arg-rich protein [Arabidopsis thaliana] "isoleucyl-tRNA synthetase, cytoplasmic (isoleucine--tRNA ligase) (ILERS) ; (AB004538) isoleucyl-tRNA synthetase, cytoplasmic [Schizosaccharomyces pombe] ; (AL022072) isoleucyl-trna synthetase, cytoplasmic [Schizosaccharomyces pombe] " (U41624) contains EGF-like repeats; similar to C. elegans protein D1044.3 [Caenorhabditis elegans] (Y16104) replicase protein [Physalis mottle tymovirus]
17334	ENU01128	ANI61C9488: 56-75 164..583	56-75	412-433	TPEST			62	0.000000	002		
17335	ENU01129	ANI61C4718: 43-62 1049..1697	43-62	406-423	TPEST			44	0.0005			
17336	ENU01130	ANI61C1041: 49-73 9:958..1395	49-73	426-444	TPEST			33	1.3			
17337	ENU01131	ANI61C8459: 43-70 2225..2664	43-70	421-440	TPEST			87	8E-17			
17338	ENU01132	ANI61C3284: 66-85 1298..1739	66-85	446-465	TPEST			31	3.8			
17339	ENU01133	ANI61C3633: 64-83 1231..1672	64-83	444-463	TPEST			32	2.2			

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17340	ENU01134	ANI61C146:3 353..3798	44-63	428-447	TPEST									(X95665) cDNA6 [Brugia pahangi]
17341	ENU01135	ANI61C1097 71-90		458-477	TPEST				31	3.9				(U31364) envelope glycoprotein gp120 [Human immunodeficiency virus type 1]
17342	ENU01136	ANI61C4927: 4:3870..3422 2707..2253	67-86	451-479	TPEST				31	5.2				
17343	ENU01137	ANI61C9105: 324..780	41-60	436-455	TPEST				54	0.000000				mitochondrial inheritance component MDM12 ; (U64674) mitochondrial inheritance component Mdm12p [Schizosaccharomyces pombe]
17344	ENU01138	ANI61C1096 4:2276..2732	26-48	421-440	TPEST				34	0.61				(Z94121) hypothetical protein Rv3903c [Mycobacterium tuberculosis]
17345	ENU01139	ANI61C1439: 1444..1654	23-42	421-440	TPEST				31	4.1				"Sex-determining transformer protein 2 precursor ; cell communication-mediating membrane protein pTra2A - Caenorhabditis elegans ; (S42187) pTra2A=membrane protein mediating cell communication [Caenorhabditis elegans, Peptide, 1475 aa]
17346	ENU01140	ANI61C6152: 3576..4040	49-71	439-471	TPEST									[Caenorhabditis elegans] ; (M91371) membrane protein [Caenorhabditis elegans] "
17347	ENU01141	ANI61C6102: 276..740	46-66	449-468	TPEST				32	1.8				hypothetical protein MJ0416 ; hypothetical protein MJ0416 - Methanococcus jannaschii ; (U67493) M. jannaschii predicted coding region MJ0416 [Methanococcus jannaschii] (AE001284) hypothetical protein [Chlamydia trachomatis] (AF044209) nuclear receptor co-repressor N-CoR [Homo sapiens] (AL022268) putative kinase/phosphohydrolase [Streptomyces coelicolor] (U97194) weak similarity to the triple-helical domain of collagens [Caenorhabditis elegans]
17348	ENU01142	ANI61C15:15 66..1100	38-58	441-462	TPEST				31	4.1				
17349	ENU01143	ANI61C1146 1:2569..3036	39-61	445-464	TPEST				34	0.82				
17350	ENU01144	ANI61C1043 5:6035..6502	56-75	462-481	TPEST				31	4.1				
17351	ENU01145	ANI61C3709: 2945..3415	49-68	459-478	TPEST				32	2.4				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
17352	ENU01146	ANI61C6857: 25-44 1391..1501	48-67	459-478	TPEST			34	0.48				(U70378) envelope polyprotein [Feline leukemia virus]
17353	ENU01147	ANI61C6835: 2443..2915	22-48	434-453	TPEST			66	1E-10				(Z99168) 40s ribosomal protein [Schizosaccharomyces pombe]
17354	ENU01148	ANI61C6874: 636..1109	22-43	444-463	TPEST			32	3.3				GATA binding factor-1A (transcription factor XGATA-1A) ; transcription factor GATA-1A - African clawed frog ; (M76566) GATA binding factor-1 [Xenopus laevis]
17356	ENU01150	ANI61C8642: 742..1226	27-46	450-469	TPEST			31	5.7				(AF036486) replication protein [Plasmid pNZ4000]
17357	ENU01151	ANI61C8646: 1626..2111	22-48	446-465	TPEST			39	0.026				DNA-directed RNA polymerase II largest subunit (RPB1)
17358	ENU01152	ANI61C1065 9:1045..1535	25-44	454-473	TPEST			30	10				(Z46935) weak similarity to conglutin (PIR accession number A33090); cDNA EST EMBL: T01355 comes from this gene; cDNA EST yk383f3.3 comes from this gene [Caenorhabditis elegans]
17359	ENU01153	ANI61C8133: 993..496	72-91	504-527	TPEST			67	1E-10				(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
17360	ENU01154	ANI61C1904: 126..660	31-50	504-523	TPEST			32	3.8				(AC004146) Hypothetical protein [Arabidopsis thaliana]
17361	ENU01155	ANI61C7675: 5031..4491	63-82	541-561	TPEST			32	3.9				(AB001347) brain beta 3 spectrin [Rattus norvegicus]
17362	ENU01156	ANI61C8356: 3042..2478	35-54	535-557	TPEST			76	3E-28				"dismutase,Mn superoxide [Saccharomyces cerevisiae]"
17363	ENU01157	ANI61C3552: 812..198	53-72	597-625	TPEST			56	3E-15				(AF047694) glutaredoxin [Vernicia fordii]
17364	ENU01158	ANI61C1713: 194..1196	60-79	1001-1020	TPEST			112	5E-24				"ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae]"

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17365	ENU01159	ANI61C5740: 26-54 325..666	26-54	303-325	TPEST				32	1.9			hypothetical zinc finger protein ZK112.2 in chromosome III ; ZK112.2 protein - Caenorhabditis elegans ; (L14324) homology with xnf7 gene product of Xenopus laevis; putative [Caenorhabditis elegans] ; (AF047027) B box zinc finger protein Ncl-1 [Caenorhabditis elegans]
17366	ENU01160	ANI61C4514: 64-85 123..474	64-85	352-373	TPEST			58	0.000000	03			homocitrate dehydratase ; LYS7 protein - yeast (Saccharomyces cerevisiae) ; (U17378) Lys7p [Saccharomyces cerevisiae] ; (Z48502) unknown [Saccharomyces cerevisiae] ; LYS7 gene [Saccharomyces cerevisiae] (U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
17367	ENU01161	ANI61C1020 53-74 7:3388..3022	53-74	358-377	TPEST			218	1E-56				"Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emericella nidulans] ; dehydrogenase, aldehyde [Emericella nidulans]"
17368	ENU01162	ANI61C4777: 41-60 602..972	41-60	350-369	TPEST			65	2E-10				"glycine cleavage system H protein ; glycine cleavage system protein H - Escherichia coli ; (M57690) H-protein [Escherichia coli] ; (X73958) H protein [Escherichia coli] ; (U28377) ORF_f129 [Escherichia coli] ; (AE000374) in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor [Escherichia coli]"
17369	ENU01163	ANI61C8131: 22-48 716..1093	22-48	338-357	TPEST			38	0.023				
17370	ENU01164	ANI61C3265: 28-47 855..1246	28-47	358-377	TPEST								
17371	ENU01165	ANI50C9281 22-46 _1:81..484	22-46	364-383	TPEST								
17372	ENU01166	ANI61C5234: 35-54 1329..926	35-54	372-396	TPEST			31	3.3				bride of sevenless precursor - fruit fly (Drosophila melanogaster)

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17373	ENU01167	ANI61C1395:	22-57	2335..2745	371-390	TPEST				32	1.5			"(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA...") (L34120) maturase [Chrysosplenium iowense] (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus] (Z99125) hypothetical protein MLC536.10 [Mycobacterium leprae] (AE001455) APOLPOprotein N-acyltransferase [Helicobacter pylori J99]
17374	ENU01168	ANI50C392_	22-41	1:327..740	373-393	TPEST				31	4.5			
17375	ENU01169	ANI61C8729:	71-90	1331..1741	424-443	TPEST				34	0.63			
17376	ENU01170	ANI61C1146	25-44	2:3984..4400	380-399	TPEST				32	2.7			
17377	ENU01171	ANI61C8297:	70-89	459..553	435-454	TPEST								
17378	ENU01172	ANI61C6475:	22-46	1146..711	389-415	TPEST				33	0.96			
17379	ENU01173	ANI61C9506:	72-91	1442..1881	449-469	TPEST				34	0.75			
17380	ENU01174	ANI61C1078	33-52	7:1158..1597	411-430	TPEST				31	6.5			
17381	ENU01175	ANI61C8580:	33-52	7426..6986	410-431	TPEST				96	2E-19			
17382	ENU01176	ANI61C4227:	34-54	548..989	410-433	TPEST				31	3.8			
17383	ENU01177	ANI61C8167:	23-42	688..1130	403-423	TPEST				38	0.051			
17384	ENU01178	ANI61C2132:	35-54	6703..6260	417-436	TPEST				36	0.15			
17385	ENU01179	ANI50C1_19	49-80	04:109..552	431-450	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17386	ENU01180	ANI61C1878: 814..1258	42-61	424-444	TPEST				43	0.001			DNA-directed RNA polymerase III 36 KD polypeptide (C34) ; DNA-directed RNA polymerase (EC 2.7.7.6) III chain C34 - yeast (Saccharomyces cerevisiae) ; (X63746) DNA dependent RNA polymerase c(III) subunit c34 [Saccharomyces cerevisiae] ; (X77395) RNA polymerase III [Saccharomyces cerevisiae] ; (Z71618) ORF YNR003c [Saccharomyces cerevisiae]
17387	ENU01181	ANI61C1093 0:756..891	58-78	443-462	TPEST				30	8.6			OP protein - Kennedy yellow mosaic virus ; (D00637) ORF for overlapping protein [Kennedy yellow mosaic virus]
17388	ENU01182	ANI61C1062 6:825..1273	66-85	445-472	TPEST				62	2E-21			ISN1 protein ; hypothetical protein YJR091c - yeast (Saccharomyces cerevisiae) ; (L43493) Isn1 gene product [Saccharomyces cerevisiae] ; (Z49591) ORF YJR091c [Saccharomyces cerevisiae]
17389	ENU01183	ANI61C1029 5:1420..1870	26-45	414-433	TPEST				33	1.3			hypothetical protein - Neurospora crassa
17390	ENU01184	ANI61C4085: 22-57 2934..3384	22-57	410-430	TPEST				31	3.9			lipase modulator precursor (LIPase helper protein) ; (D50588) lipase modulator protein [Pseudomonas aeruginosa] ; (AB008452) proposal modulator or activator protein for lipase [Pseudomonas aeruginosa]
17391	ENU01185	ANI61C8185: 1518..1068	28-56	416-436	TPEST				81	4E-15			"hypothetical 36.8 KD protein C26A3.16 in chromosome I ; (Z69240) yeast dsk2 homolog, ubiquitin-like protein [Schizosaccharomyces pombe]
17392	ENU01186	ANI61C7357: 59-78 805..355	59-78	447-467	TPEST								
17393	ENU01187	ANI61C3768: 22-55 171..621	22-55	409-430	TPEST								

Gene annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17394	ENU01188	ANI61C7771: 22-47 3089..2638		409-431	TPEST				229	1E-59			probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emericella nidulans] (AF087280) (N-acetylneuraminyl)-galactosylglucosylceramide N-acetyl/galactosaminyl transferase [Chlamydia trachomatis] (AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae] (AL023780) putative mrna stability protein [Schizosaccharomyces pombe] Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae] (AC006413) hypothetical protein [Arabidopsis thaliana] (U08029) NADH:nitrate reductase [Spinacia oleracea] (D45163) embryonic muscle myosin heavy chain [Halocynthia roretzi] (AL049485) putative squalene-hopene cyclase [Streptomyces coelicolor] amidase (EC 3.5.1.4) - Aspergillus oryzae ; (D10492) acetamidase [Aspergillus oryzae] (U12978) BS-84 [Homo sapiens]
17395	ENU01189	ANI61C4061: 22-41 1295..1746		412-431	TPEST				31	6.7			
17396	ENU01190	ANI61C9579: 25-47 2756..2651		416-435	TPEST				132	1E-30			
17397	ENU01191	ANI61C7353: 41-62 5766..6218		431-451	TPEST				50	0.00001			
17398	ENU01192	ANI61C3827: 39-61 108..560		427-449	TPEST				49	0.00002			
17399	ENU01193	ANI61C7142: 44-63 462..915		436-455	TPEST				31	6.7			
17400	ENU01194	ANI61C1079 40-59 9:353..807		431-452	TPEST				30	8.9			
17401	ENU01195	ANI61C873:7 40-60 77..1231		430-452	TPEST				31	4			
17402	ENU01196	ANI61C7089: 22-48 391..845		415-434	TPEST				32	3			
17403	ENU01197	ANI61C7024: 66-85 307..762		447-479	TPEST				35	0.35			
17404	ENU01198	ANI61C5486: 49-68 363..819		440-463	TPEST				31	5.2			
17405	ENU01199	ANI61C6338: 38-58 1079..1535		433-452	TPEST				32	1.8			putative aspartate aminotransferase 1 (transaminase A) (ASPAT) ; aspartate transaminase (EC 2.6.1.1) - Methanococcus jannaschii ; (U67459) aspartate aminotransferase (aspB1) [Methanococcus jannaschii] (AF033210) major surface glycoprotein [Pneumocystis carinii f. sp. hominis] (AF015193) NADH dehydrogenase subunit 4 [Onchocerca volvulus] (Y14157) Toucan protein [Drosophila melanogaster]
17406	ENU01200	ANI61C7622: 60-79 1109..653		454-474	TPEST				30	8.9			
17407	ENU01201	ANI61C623:1 40-61 84..641		433-455	TPEST				31	6.9			
17408	ENU01202	ANI61C1042 22-47 7:1510..1053		418-437	TPEST				37	0.07			

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17409	ENU01203	ANI61C9327: 22-48 2055..2512		413-437	TPEST				31	4			(AF078788) similar to Batten disease-related protein CLN3 [Caenorhabditis elegans] COI intron 10 protein - Podospora anserina mitochondrion (SGC3) ; (X55026) Dod COI i10 grp IB protein [Podospora anserina]
17410	ENU01204	ANI61C1083: 22-52 560..1017		418-437	TPEST				31	6.9			
17411	ENU01205	ANI61C7776: 22-53 3365..3823		419-438	TPEST								
17412	ENU01206	ANI61C5075: 59-76 563..1022		450-476	TPEST								
17413	ENU01207	ANI61C1119: 27-46 848..730		423-445	TPEST				32	2.4			Ig heavy chain V region (129) - mouse
17414	ENU01208	ANI50C1088 6_1:213..674		422-441	TPEST				31	6.9			acidic protein - Caenorhabditis elegans (fragment) ; (M77697) acid-rich protein [Caenorhabditis elegans] "(AF004668) Sia alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase [Homo sapiens] "
17415	ENU01209	ANI61C8837: 22-47 2185..2647		423-442	TPEST				31	6.9			"Dihydrolipoamide dehydrogenase precursor ; dihydrolipoamide dehydrogenase (EC 1.8.1.4) precursor - yeast (Saccharomyces cerevisiae) ; (J03645) dihydrolipoamide dehydrogenase [Saccharomyces cerevisiae] ; (M20880) lipoamide dehydrogenase [Saccharomyces cerevisiae] ; (Z46255) lpd1, dhip1, len: 499. CAl: 0.26, DLDH_YEAST P09624 dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae] ; (D50617) dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae] ; (D44596) lipoamide dehydrogenase [Saccharomyces cerevisiae] "
17416	ENU01210	ANI61C6002: 22-43 1181..1644		424-443	TPEST				110	5E-24			Neural-cadherin 2 precursor (N-cadherin 2) ; N-cadherin 2 precursor - African clawed frog ; (X57675) N-cadherin [Xenopus laevis]
17417	ENU01211	ANI61C1140 7:2457..2920		458-477	TPEST				31	5.4			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17418	ENU01212	ANI61C7170: 2840..3304	34-53	437-456	TPEST				109	8E-24			40S ribosomal protein S9 (S7) ; (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]
17419	ENU01213	ANI61C8617: 384..850	22-49	426-445	TPEST				139	8E-33			"probable 3-hydroxybutyryl-CoA dehydrogenase (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD) ; (U29084) similar to Clostridium acetobutylicum NAD-dependent beta-hydroxybutyryl-CoA dehydrogenase, PIR Accession Number A43723 [Bacillus subtilis] "
17420	ENU01214	ANI61C6250: 562..1029	23-42	429-448	TPEST			31	5.4				"(AL031866) ORF8, len: 255 aa, hufC, highly similar to histidine utilization repressor from P22773 Pseudomonas putida, 63.2% identity in 242 aa overlap, Fasta scores opt: 1022, E(0.0. [Yersinia pestis] "
17421	ENU01215	ANI61C6358: 283..750	22-52	428-447	TPEST			33	1.1				complement C3d/Epstein-Barr virus receptor precursor - human
17422	ENU01216	ANI50C3036 9 2:215..682	38-57	443-463	TPEST			34	0.48				(D64052) cytochrome P450 like_ TBP [Nicotiana tabacum]
17423	ENU01217	ANI61C1071 9:530..998	38-57	445-464	TPEST			34	0.62				(Z82256) cDNA EST yk251g7.3 comes from this gene; cDNA EST yk251g7.5 comes from this gene; cDNA EST comes from this gene; cDNA EST EMBL:D68223 comes from this gene; cDNA EST EMBL:C12737 comes from this gene; cDNA EST yk389c8.5 comes from this gene; cDNA EST ...
17424	ENU01218	ANI61C1011: 1883..2351	53-73	453-479	TPEST			98	3E-20				het-c2 protein - Podospora anserina ; (U05236) HET-C2 [Podospora anserina]
17425	ENU01219	ANI61C1189: 5906..6375	22-56	430-449	TPEST			33	1.4				Aflatoxin biosynthesis polyketide synthase (PKS) ; (L42765) polyketide synthase [Aspergillus parasiticus] ; (L42766) polyketide synthase [Aspergillus parasiticus] ; polyketide synthase [Aspergillus parasiticus]
17426	ENU01220	ANI61C3019: 744..1213	52-72	449-479	TPEST								
17427	ENU01221	ANI61C5910: 913..1384	48-67	453-477	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
17428	ENU01222	ANI61C8200: 22-53 2736..3208	22-53	433-452	TPEST						31	7.2	"probable 3',5'-cyclic phosphodiesterase R08D7.6 ; (Z12017) predicted using GeneFinder; similar to cyclic GMP phosphodiesterases; cDNA EST EMBL:D32815 comes from this gene; cDNA EST EMBL:D33365 comes from this gene; cDNA EST EMBL:D36169 comes from this gene; cDNA EST EMBL:D3369.. "
17429	ENU01223	ANI61C6431: 22-45 39..511	22-45	420-452	TPEST								(AL021711) putative protein [Arabidopsis thaliana]
17430	ENU01224	ANI61C4316: 39-62 323..796	39-62	449-470	TPEST						32	1.9	"(Z98551) predicted using hexExon; MAL3P6.11 (PFC0760c), Hypothetical protein, len: 3395 aa [Plasmodium falciparum] "
17431	ENU01225	ANI61C3867: 22-47 1884..2358	22-47	433-454	TPEST						30	9.5	(AE000829) unknown [Methanobacterium thermoautotrophicum]
17432	ENU01226	ANI61C7073: 47-67 5143..5617	47-67	458-479	TPEST						30	9.5	ATP-dependent RNA helicase DBP7 ; probable purine nucleotide-binding protein YKR024c - yeast (Saccharomyces cerevisiae) ; (Z28249) ORF YKR024c [Saccharomyces cerevisiae]
17433	ENU01227	ANI61C1804: 46-66 223..698	46-66	449-479	TPEST						77	8E-14	ribosomal protein S27 (metallopanstimulin 1) ; 40S ribosomal protein S27 (metallopan-stimulin 1) (MPS-1) ; growth factor-inducible zinc finger protein MPS-1 - human ; (L19739) metallopanstimulin [Homo sapiens] ; (U57847) ribosomal protein S27 [Homo sapiens]
17434	ENU01228	ANI61C6494: 46-68 5210..5685	46-68	452-479	TPEST						32	3.2	(X66593) apocytichrome B [Pichia pipieri]
17435	ENU01229	ANI50C3665 27-46 0_1:99..574	27-46	441-460	TPEST								
17436	ENU01230	ANI61C3327: 28-48 630..154	28-48	443-462	TPEST								
17437	ENU01231	ANI61C1110 51-78 7:6219..6695	51-78	465-485	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17438	ENU01232	ANI61C8963: 43-71	453-477	TPEST									
17439	ENU01233	ANI61C3345: 27-49	439-462	TPEST									Focal adhesion kinase 1 (FADK 1) (PP125FAK) ; (AF020777) focal adhesion kinase; pp125FAK [Rattus norvegicus]
17440	ENU01234	ANI61C1113 39-59	454-475	TPEST									(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
17441	ENU01235	ANI61C9369: 22-51	439-459	TPEST									(Z34814) voltage-dependent L-type Ca channel alpha 1 subunit [Homo sapiens]
17442	ENU01236	ANI61C8497: 23-58	438-461	TPEST									(AL049558) putative phosphatidylinositol-kinase [Schizosaccharomyces pombe]
17443	ENU01237	ANI61C7016: 36-59	455-474	TPEST									ubiquinone biosynthesis monooxygenase COQ6 ; hypothetical protein YGR255c - yeast (Saccharomyces cerevisiae) ; (Z73040) ORF YGR255c [Saccharomyces cerevisiae] ; (X99228) G9165 [Saccharomyces cerevisiae] ; (AF003698) COQ6 monooxygenase [Saccharomyces cerevisiae]
17444	ENU01238	ANI61C4368: 23-51	443-462	TPEST									(AF070999) tetracycline resistance protein [IncQ plasmid pIE1120]
17445	ENU01239	ANI61C9514: 39-58	453-479	TPEST									(L15365) stage specific activator protein; SSAP [Strongylocentrotus purpuratus]
17446	ENU01240	ANI61C5951: 24-57	443-464	TPEST									
17447	ENU01241	ANI61C1810: 22-41	443-463	TPEST									
17448	ENU01242	ANI61C9348: 52-71	467-494	TPEST									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17449	ENU01243	ANI61C5968: 25-44 413..899	448-469	448-469	TPEST			41	0.007				S-adenosylmethionine synthetase (methionine adenosyltransferase) (ADOMET synthetase) ; methionine adenosyltransferase (EC 2.5.1.6) - Neurospora crassa ; (U21547) S-adenosylmethionine synthetase [Neurospora crassa] ; Met(S-adenosyl) synthetase [Neurospora crassa] probable membrane protein YPL134c - yeast (Saccharomyces cerevisiae) ; (U43703) Lpi11p [Saccharomyces cerevisiae]
17450	ENU01244	ANI50C6889 _1:811..1300	57-76	484-504	TPEST			112	1E-24				(AL022103) histidyl-tma synthetase [Schizosaccharomyces pombe]
17451	ENU01245	ANI61C2652: 22-45 538..1028	450-470	450-470	TPEST			72	3E-12				"acid phosphatase (EC 3.1.3.2) AcpH-1 precursor, lysosomal - fruit fly (Drosophila melanogaster) "
17452	ENU01246	ANI61C8330: 22-54 422..912	451-470	451-470	TPEST			31	5.8				(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]
17453	ENU01247	ANI61C6392: 22-52 1606..1115	452-471	452-471	TPEST			31	5.8				(Y08257) orf c04030 [Sulfolobus solfataricus]
17454	ENU01248	ANI61C1118 5:9614..10105	25-49	455-474	TPEST			31	4.4				(Z81095) cDNA EST yk421g8.3 comes from this gene; cDNA EST yk421g8.5 comes from this gene; cDNA EST yk449e1.5 comes from this gene [Caenorhabditis elegans]
17455	ENU01249	ANI61C8898: 28-50 487..979	455-478	455-478	TPEST			31	4.4				
17456	ENU01250	ANI61C2666: 29-48 673..1165	458-479	458-479	TPEST			31	4.4				
17457	ENU01251	ANI61C9112: 22-48 3526..4018	453-472	453-472	TPEST			31	4.4				
17458	ENU01252	ANI61C1116 3:2713..3206	22-52	452-473	TPEST			31	4.4				
17459	ENU01253	ANI61C8609: 28-63 70..563	28-63	449-479	TPEST			31	4.4				
17460	ENU01254	ANI61C1754: 23-58 1628..2122	23-58	456-475	TPEST			32	3.4				(U66846) orf5 [Streptococcus pneumoniae]
17461	ENU01255	ANI61C8431: 28-49 367..861	28-49	458-480	TPEST			102	5E-25				probable chorismate mutase (CM) ; (Z98529) putative chorismate mutase [Schizosaccharomyces pombe]

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17462	ENU01256	ANI61C9659: 26-45	458-479	458-479	TPEST								chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans ; (D21269) chitin synthase [Emericella nidulans] ; (D83216) chitin synthase B [Emericella nidulans] ; chitin synthetase [Emericella nidulans]
17463	ENU01257	ANI61C1188: 25-46	450-479	450-479	TPEST			83	1E-15				[Emericella nidulans] (AE001593) L11 Ribosomal Protein [Chlamydia pneumoniae]
17464	ENU01258	ANI61C5136: 22-50	457-476	457-476	TPEST			32	3.5				kinesin-like protein KIF4 ; microtubule-associated motor KIF4 - mouse ; (D12646) KIF4 [Mus musculus]
17465	ENU01259	ANI61C5180: 22-54	443-476	443-476	TPEST			42	0.003				"112.3 KD protein in PYK1-SNC1 intergenic region ; FUN12 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Fun12p: 97kDa protein, function unknown [Saccharomyces cerevisiae]"
17466	ENU01260	ANI61C8540: 22-52	457-476	457-476	TPEST			39	0.027				(U53180) coded for by C. elegans cDNA CEMSE31F; Similar to alpha-SNAP protein [Caenorhabditis elegans] (L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
17467	ENU01261	ANI61C4234: 22-50	458-477	458-477	TPEST			31	7.8				Alcohol dehydrogenase II
17468	ENU01262	ANI61C5359: 22-48	451-477	451-477	TPEST			34	0.52				(AF139463) early growth response 2 protein [Homo sapiens]
17469	ENU01263	ANI61C8971: 22-48	453-478	453-478	TPEST			31	4.6				(AB011141) KIAA0569 protein [Homo sapiens]
17470	ENU01264	ANI61C1025 23-49	458-479	458-479	TPEST								
17471	ENU01265	ANI61C5977: 22-54	449-478	449-478	TPEST								
17472	ENU01266	ANI61C3031: 22-55	458-478	458-478	TPEST								
17473	ENU01267	ANI61C1094 48-67	485-504	485-504	TPEST								
17474	ENU01268	ANI61C1139 22-48	462-479	462-479	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17475	ENU01269	ANI61C5317: 22-50 2883..2384	22-50	448-479	TPEST			81	81	4E-15			PSI protein ; DNAJ-like protein homolog - fission yeast (Schizosaccharomyces pombe) ; (L37753) Psi protein [Schizosaccharomyces pombe] ; DnaJ-like protein [Schizosaccharomyces pombe]
17476	ENU01270	ANI61C3239: 22-56 275..774	22-56	449-479	TPEST			31	31	6			transforming growth factor-beta type III receptor - chicken ; (L01121) transforming growth factor-beta type III receptor [Gallus gallus] (X57581) coat protein [Bamboo mosaic virus] ; (D26017) ORF5=25k; encodes the coat protein [Bamboo mosaic virus]
17477	ENU01271	ANI61C404:4 052..3553	22-51	449-479	TPEST			32	32	3.5			hypothetical protein YOR281c - yeast (Saccharomyces cerevisiae) ; (X89633) hypothetical protein [Saccharomyces cerevisiae] ; (Z75189) ORF YOR281c [Saccharomyces cerevisiae]
17478	ENU01272	ANI61C1089 8:650..1149	22-52	457-479	TPEST			38	38	0.035			potential proteasome component C5 (multicatalytic endopeptidase complex subunit C5) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRS3 - yeast (Saccharomyces cerevisiae) ; (M34777) proteasome subunit [Saccharomyces cerevisiae] ; (D00845) proteasome subunit [Saccharomyces cerevisiae] ; (X78214) PRS3 [Saccharomyces cerevisiae] ; (Z35802) ORF YBL041w [Saccharomyces cerevisiae]
17479	ENU01273	ANI61C1084: 22-54 1095..1594	22-54	447-479	TPEST			169	169	8E-42			(D64056) LMP7 of nurse shark [Ginglymostoma cirratum] RIBOnuclease E (RNase E) (Z95398) unknown [Mycobacterium leprae]
17480	ENU01274	ANI61C3960: 22-54 108..607	22-54	449-479	TPEST			32	32	2.7			
17481	ENU01275	ANI61C4862: 22-44 1434..1933	22-44	449-479	TPEST			32	32	2			
17482	ENU01276	ANI61C9745: 22-49 3851..4350	22-49	460-479	TPEST			31	31	6			
17483	ENU01277	ANI61C9978: 26-45 2987..2487	26-45	458-484	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17484	ENU01278	ANI61C9255: 394..898	66-85	509-528	TPEST				64	5E-10		hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae]
17485	ENU01279	ANI61C319:3 472..2960	24-56	472-494	TPEST				53	2E-15		putative carboxymethylglutaminyl hydrolase (dienehydrolase) (DLH) ; hypothetical protein YDL086w - yeast (Saccharomyces cerevisiae) ; (Z74134) ORF YDL086w [Saccharomyces cerevisiae]
17486	ENU01280	ANI61C8494: 1258..1770	59-78	507-529	TPEST				102	2E-38		hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region ; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe13p [Saccharomyces cerevisiae]
17487	ENU01281	ANI61C7555: 3253..3767	49-69	486-521	TPEST				32	2.2		(X92761) VP1 RNA polymerase [Infectious bursal disease virus]
17488	ENU01282	ANI61C1123 2:3621..4141	62-97	513-540	TPEST				38	0.0000004		hypothetical 71.3 KD protein in SCM4-MUP1 intergenic region ; hypothetical protein YGR054w - yeast (Saccharomyces cerevisiae) ; (Z72839) ORF YGR054w [Saccharomyces cerevisiae]
17489	ENU01283	ANI61C1024 7:3693..3172	30-49	490-509	TPEST				38	0.0000004		hypothetical 64.5 KD protein in COX4-GTS1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae) ; (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae] ; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]
17490	ENU01284	ANI61C134:4 274..4798	23-50	485-504	TPEST				31	4.9		(Z78542) predicted using GeneFinder; similar to cuticlin [Caenorhabditis elegans]
17491	ENU01285	ANI61C7388: 4097..4622	63-82	518-546	TPEST				38	0.0000004		hypothetical 64.5 KD protein in COX4-GTS1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae) ; (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae] ; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]
17492	ENU01286	ANI61C3381: 634..1161	50-69	500-535	TPEST				31	4.9		(Z78542) predicted using GeneFinder; similar to cuticlin [Caenorhabditis elegans]

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17493	ENU01287	ANI61C9600: 4057..4585	27-47	494-513	TPEST				151	4E-36			hypothetical oxidoreductase in APRE-COMK intergenic region (ORFX) ; (Y14084) hypothetical protein [Bacillus subtilis] ; (Z99109) similar to alcohol dehydrogenase [Bacillus subtilis]
17494	ENU01288	ANI61C9874: 23-43	23-43	489-510	TPEST			31	8.5				(U93416) RXR [Anemonia sulcata]
17495	ENU01289	ANI61C4254: 32-52	32-52	501-520	TPEST			32	2.2				(AF05368) heat shock protein DnaJ homolog [Vibrio harveyi]
17496	ENU01290	ANI61C4296: 22-54	22-54	491-511	TPEST			31	8.5				(AF080235) glycosyl transferase homolog [Streptomyces cyanogenus]
17497	ENU01291	ANI61C8256: 23-52	23-52	497-517	TPEST			105	3E-22				(U40843) ORFS8; Method: conceptual translation supplied by author. [Saccharomyces cerevisiae]
17498	ENU01292	ANI61C6581: 38-57	38-57	509-537	TPEST			58	0.000000	05			heterogeneous nuclear ribonucleoprotein K ; transformation upregulated nuclear protein - human ; (X72727) transformation upregulated nuclear protein [Homo sapiens]
17499	ENU01293	ANI61C9637: 61-80	61-80	548-567	TPEST			173	8E-43				Peptidyl-prolyl cis-trans isomerase (PPase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
17500	ENU01294	ANI61C8828: 42-62	42-62	529-552	TPEST			37	0.0007				(U43281) Lpg18p [Saccharomyces cerevisiae]
17501	ENU01295	ANI61C8803: 27-46	27-46	515-539	TPEST			34	0.79				(Z81523) similar to Myb DNA-binding proteins (2 domains); cDNA EST yk300c3.5 comes from this gene [Caenorhabditis elegans]
17502	ENU01296	ANI61C7538: 25-44	25-44	525-544	TPEST			55	0.000000	4			(AF021797) peroxisomal receptor for PTS2-containing proteins Pex7p [Pichia pastoris]

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17503	ENU01297	ANI61C7165: 25-44 1783..1218	25-44	522-548	TPEST				34	0.62			hypothetical 9.1 KD protein C23C11.12 in chromosome I; (Z98559) very hypothetical protein [Schizosaccharomyces pombe]
17504	ENU01298	ANI61C953:1 812..1243	22-47	522-549	TPEST				71	5E-12			"ATP synthase alpha chain, mitochondrial precursor; H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Neurospora crassa; (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa]"
17505	ENU01299	ANI61C3229: 22-51 1354..1925	22-51	520-551	TPEST				106	2E-22			"ubiquitin / ribosomal protein CEP52 - yeast (Saccharomyces cerevisiae); (X05728) ubiquitin [Saccharomyces cerevisiae]; (X05729) ubiquitin [Saccharomyces cerevisiae]; (X73541) UBI2 [Saccharomyces cerevisiae]; (Z28319) ORF YKR094c [Saccharomyces cerevisiae]; (Z38059) ubi1, len: 128, CAl: 0.74, spliced, S34428 S34428 ubiquitin-52 amino acid fusion protein [Saccharomyces cerevisiae]"
17506	ENU01300	ANI61C2576: 46-74 492..1065	46-74	545-577	TPEST				76	1E-16			ubiquitin-like protein SMT3; SMT3 protein - yeast (Saccharomyces cerevisiae); (U27233) Smt3p [Saccharomyces cerevisiae]; (U33057) suppressor of MIF2 mutations; CAl: 0.31 [Saccharomyces cerevisiae]
17507	ENU01301	ANI61C2666: 24-43 3325..3907	24-43	544-564	TPEST				32	2.5			light repressible receptor protein kinase - Arabidopsis thaliana; (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]
17508	ENU01302	ANI61C2751: 26-50 280..881	26-50	564-585	TPEST				32	3.5			(AB007769) polygalacturonase B [Aspergillus oryzae]
17509	ENU01303	ANI61C1001: 29-48 9:3435..4045	29-48	566-597	TPEST				35	0.4			(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]
17510	ENU01304	ANI61C5388: 31-50 1023..1634	31-50	569-600	TPEST								

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17511	ENU01305	ANI61C8549: 22-41 3074..3690		569-596	TPEST				34	1.2			hypothetical 15.6 KD protein in CSN-ADHB intergenic region ; (U93875) Yra1 [Bacillus subtilis] ; (X92868) unknown [Bacillus subtilis] ; (Z99117) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] ubiquitin-conjugating enzyme E2-23 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) ; 23K ubiquitin carrier protein E2 - wheat ; (M28059) ubiquitin carrier protein [Triticum vulgare]
17512	ENU01306	ANI61C5686: 22-42 104..729		578-605	TPEST				34	0.091			hypothetical 8.2 KD protein C26A3.14C in chromosome I ; (Z69240) very hypothetical protein [Schizosaccharomyces pombe] (AF032382) metalloprotease-disintegrin [Xenopus laevis] ARP2/3 complex 21 KD subunit (P21-ARC) ; hypothetical protein YLR370c - yeast (Saccharomyces cerevisiae) ; (U19103) Ylr370cp [Saccharomyces cerevisiae] (AF097832) malonyl-CoA decarboxylase precursor [Homo sapiens] (AF084484) putative outer membrane protein [Helicobacter pylori]
17513	ENU01307	ANI61C7805: 59-78 4634..5266		629-649	TPEST				40	0.016			(M17199) Fus1 fusion peptide [Saccharomyces cerevisiae] ; (M16717) FUS1 protein [Saccharomyces cerevisiae] (AB006188) acidic class III chitinase OsChib3a [Oryza sativa]
17514	ENU01308	ANI61C3240: 62-82 4092..4852		752-780	TPEST				32	4.6			
17515	ENU01309	ANI61C1058 23-47 9:6896..6386		248-275	TPEST	cluster1512_1			29	0.052	99		
17516	ENU01310	ANI61C9440: 30-49 741..53		204-226	TPEST	cluster1544_1			30	2.9	99		
17517	ENU01311	ANI61C4443: 444..1			TPEST	cluster296_1			29	5.9	99		
17518	ENU01312	ANI61C6466: 104-130 1857..1207		274-293	TPEST	cluster1763_1			32	2.5	100		
17519	ENU01313	ANI61C8621: 27-48 542..310		358-385	TPEST	cluster2087_1			32	2.5	99		
17520	ENU01314	ANI61C8638: 24-51 205..371		361-388	TPEST	cluster4468_1			31	3.4	98		
17521	ENU01315	ANI61C915:7 72..1054			TPEST	cluster3413_2					100		
17522	ENU01316	ANI61C6923: 1927..1021			TPEST	cluster1947_1					99		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17523	ENU01317	ANI61C1031 3:2651..2160			TPEST	cluster1615_1					99	
17524	ENU01318	ANI61C3480: 1923..2208			TPEST	cluster1734_1					100	
17525	ENU01319	ANI61C246:1 30-51 263..1430	30-51	501-528	TPEST	cluster145_1		44	0.0007		97	A-agglutinin attachment subunit precursor ; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae]
17526	ENU01320	ANI61C1253: 513..1			TPEST	cluster197_1					99	
17527	ENU01321	ANI61C353:3 704..3055			TPEST	cluster95_1		32	0.66		100	(U02970) unknown [Prototheca wickerhamii]
17528	ENU01322	ANI61C2481: 110..1			TPEST	cluster2573_1		29	5.7		100	(Z54284) D2085.2 [Caenorhabditis elegans]
17529	ENU01323	ANI61C3543: 57-76 672..475	57-76	302-329	TPEST	cluster3142_1		66	1E-10		97	(AJ001732) rAsp f 4 [Aspergillus fumigatus]
17530	ENU01324	ANI61C1120: 478..280			TPEST	cluster3142_1		57	0.000000 05		97	60S ribosomal protein L27A (L29) (CRP1) ; ribosomal protein L27a.e - Neurospora crassa ; (X06320) put. ribosomal protein [Neurospora crassa] ; (X13254) put. ribosomal protein (AA 1-149) [Neurospora crassa]
17531	ENU01325	ANI61C1064 9:387..1121			TPEST	cluster1086_1					100	
17532	ENU01326	ANI61C1035 6:2570..2951			TPEST	cluster202_1					98	
17533	ENU01327	ANI61C3610: 22-40 106..1	22-40	162-182	TPEST	cluster5177_1		31	1.1		96	"(Z34799) predicted using Genefinder; contains a proline-rich domain, and partial similarity to RD protein; cDNA EST EMBL:M89085 comes from this gene; cDNA EST EMBL:C10105 comes from this gene; cDNA EST yk480b4.5 comes from this..."
17534	ENU01328	ANI61C5231: 22-48 281..729	22-48	430-457	TPEST	cluster1916_1		35	0.37		98	(U00066) weakly similar to notch protein in and just upstream of the poly-Gln region [Caenorhabditis elegans]

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17535	ENU01329	ANI61C7657: 702..1535	22-48	200-219	TPEST	cluster1739_1					99	
17536	ENU01330	ANI61C6509: 746..203	24-43	275-297	TPEST	cluster82_1		33	0.49		100	(U41293) unknown [Saccharomyces cerevisiae]
17537	ENU01331	ANI61C5234: 1171..663			TPEST	cluster5_1					98	
17538	ENU01332	ANI61C6237: 1..581			TPEST	cluster9200_1					99	
17539	ENU01333	ANI61C1073: 0:121..1			TPEST	cluster1562_1					100	
17540	ENU01334	ANI61C6247: 2985..2539			TPEST	cluster2835_1					100	
17541	ENU01335	ANI61C465:7491..7090			TPEST	cluster7959_1					99	
17542	ENU01336	ANI61C8418: 1248..2036	22-43	524-551	TPEST	cluster102_1					96	
17543	ENU01337	ANI61C7015: 6784..7046			TPEST	cluster834_1					99	
17544	ENU01338	ANI61C6602: 2923..3140	102-123	473-498	TPEST	cluster5791_1		59	0.000000		99	(AL031541) putative dehydrogenase [Streptomyces coelicolor]
17545	ENU01339	ANI61C5686: 1..729	28-48	377-404	TPEST	cluster5752_1		31	5.3		100	(L20476) nicein [Mus musculus]
17546	ENU01340	ANI61C7016: 5055..5615	22-41	228-247	TPEST	cluster2753_1		32	1.3		98	"Chain C, Klebsiella Aerogenes Urease, H134a Variant "
17547	ENU01341	ANI61C5697: 1..322	27-47	173-198	TPEST	cluster8536_1		29	7		100	(Z81576) predicted using Genefinder [Caenorhabditis elegans]
17548	ENU01342	ANI61C1968: 306..654			TPEST	cluster6504_1					98	
17549	ENU01343	ANI61C7388: 5123..5205			TPEST	cluster1642_1					97	
17550	ENU01344	ANI61C1970: 110..592			TPEST	cluster1431_1					99	
17551	ENU01345	ANI61C7027: 1..485	71-98	245-272	TPEST	cluster2734_1		30	4.3		96	(Z81513) F26D2.13 [Caenorhabditis elegans]
17552	ENU01346	ANI61C8431: 212..910			TPEST	cluster6091_1					100	
17553	ENU01347	ANI61C8772: 1162..1349	26-44	810-829	TPEST	cluster2751_1		32	5.3		99	(AC004493) KIAA0324 [Homo sapiens]
17554	ENU01348	ANI61C1003: 6:462..766			TPEST	cluster5455_1					97	

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17555	ENU01349	ANI61C1129 4:174..657	31-53	169-188	TPEST	cluster3593_1		41	0.0001		100		ADP/ATP carrier protein [Candida parapsilosis]
17556	ENU01350	ANI61C1041 9:931..1432	22-42	218-240	TPEST	cluster1735_1		30	4.4		100		nikD protein - Escherichia coli; (U00039) nikD [Escherichia coli]; (AE000423) ATP-binding protein of nickel transport system [Escherichia coli]
17557	ENU01351	ANI61C1473: 3644..4570			TPEST	cluster3819_1		33	0.3		99		ISL2 protein - Lactobacillus helveticus; (X77332) mobile genetic element [Lactobacillus helveticus]
17558	ENU01352	ANI61C4167: 1..315	44-63	575-596	TPEST	cluster554_1		33	1.6		97		(AF010227) receptor-associated coactivator 3 [Homo sapiens]
17559	ENU01353	ANI61C1042 9:2617..3123			TPEST	cluster10082_1					99		(AL035521) putative protein [Arabidopsis thaliana]
17560	ENU01354	ANI61C1513: 1..189	26-45	227-246	TPEST	cluster9499_1		32	0.75		98		Ig kappa chain V-J region (T24-9) - human (fragment); (Z27174) IG light chain variable region (VJ) [Homo sapiens]
17561	ENU01355	ANI61C1044 4:166..472	39-59	421-448	TPEST	cluster2130_1		32	2.4		99		Prephenate dehydrogenase (NADP+) (PRDH); prephenate dehydrogenase (NADP+) (EC 1.3.1.13) - yeast (Saccharomyces cerevisiae); (Z36035) ORF YBR166c [Saccharomyces cerevisiae]
17562	ENU01356	ANI61C630:1 ..853	102-127	314-341	TPEST	cluster199_1		55	1E-11		99		
17563	ENU01357	ANI61C7751: 919..339			TPEST	cluster8165_1					100		
17564	ENU01358	ANI61C9283: 4849..4381	26-45	160-184	TPEST	cluster1651_1		32	1.6		100		(AC005309) unknown protein [Arabidopsis thaliana]
17565	ENU01359	ANI61C8934: 1977..1618			TPEST	cluster3049_1					99		
17566	ENU01360	ANI61C1559: 2194..1598	61-78	341-366	TPEST	cluster3480_1		30	7		99		"Pre-RRNA processing protein SRD1; SRD1 protein - yeast (Saccharomyces cerevisiae); (X06322) open reading frame (AA 1 - 225) [Saccharomyces cerevisiae]; (X59720) YCR018c, len:225 [Saccharomyces cerevisiae]"
17567	ENU01361	ANI61C584:3 47..1244	102-125	537-564	TPEST	cluster385_1		36	0.22		99		(AC000348) T7N9.12 [Arabidopsis thaliana]

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17568	ENU01362	ANI61C8479: 161..1	45-64	316-335	TPEST	cluster4886_1			32	2.4	96		(AF041382) microtubule binding protein D-CLIP-190 [Drosophila melanogaster]
17569	ENU01363	ANI61C8138: 1614..1813	49-68	410-437	TPEST	cluster7184_1			33	1.5	99		(D64015) T-cluster binding protein [Homo sapiens]
17570	ENU01364	ANI61C6322: 110..558			TPEST	cluster2601_1					97		
17571	ENU01365	ANI61C9327: 2106..2554			TPEST	cluster8203_1			30	1.9	100		(U87460) putative endothelin receptor type B-like protein [Homo sapiens]
17572	ENU01366	ANI61C7768: 303..797	66-93	391-418	TPEST	cluster1794_1			32	1.8	100		Invected protein ; homeotic protein Invected - fruit fly (Drosophila melanogaster) ; (X05273) invected gene product (AA 1-576) [Drosophila melanogaster]
17573	ENU01367	ANI61C2166: 788..1243			TPEST	cluster5837_1					99		
17574	ENU01368	ANI61C1141: 0:2511..2083	22-44	457-484	TPEST	cluster227_1					99		
17575	ENU01369	ANI61C2172: 1225..767			TPEST	cluster1042_1					98		
17576	ENU01370	ANI61C4811: 684..363	43-64	491-518	TPEST	cluster9535_1			32	4.3	100		(Z70309) R102.7 [Caenorhabditis elegans]
17577	ENU01371	ANI61C2786: 94..411			TPEST	cluster10895_1					98		
17578	ENU01372	ANI61C7142: 521..939			TPEST	cluster1887_1			32	4.7	99		(AF067216) No definition line found [Caenorhabditis elegans]
17579	ENU01373	ANI61C1045: 9:1520..936	50-74	528-547	TPEST	cluster4943_1					99		
17580	ENU01374	ANI61C1092: 8:2247..897			TPEST	cluster1312_2			29	4.5	100		(Z81560) K02E2.5 [Caenorhabditis elegans]
17581	ENU01375	ANI61C1024: 1690..1009			TPEST	cluster548_1			29	5.8	99		hypothetical 180.2 KD protein in FAA4-HOR7 intergenic region ; probable membrane protein YMR247c - yeast (Saccharomyces cerevisiae)
17582	ENU01376	ANI61C1626: 1305..426			TPEST	cluster4702_1					99		
17583	ENU01377	ANI61C2195: 708..1			TPEST	cluster1093_1			29	4.8	98		Shufflon-specific DNA recombinase ; probable integrase - Escherichia coli ; (X12577) rct protein (AA 1-384) [Escherichia coli]

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17584	ENU01378	ANI61C289:2 882..1832			TPEST	cluster445_2					99		
17585	ENU01379	ANI61C1024 2:1738..1095	68-87	297-316	TPEST	cluster46_1		31	4.6		100		(AF064823) NADH dehydrogenase subunit 2 [Sarcophyton glaucum]
17586	ENU01380	ANI61C8193: 1014..1490	53-72	391-418	TPEST	cluster9706_1		31	3.7		99		FIXR protein ; fixR protein - Bradyrhizobium japonicum ; (X06167)
17587	ENU01381	ANI61C8986: 4600..3743			TPEST	cluster1342_1					100		fixR gene product (AA 1 - 278) [Bradyrhizobium japonicum]
17588	ENU01382	ANI61C6339: 2309..1292			TPEST	cluster259_1		60		0.000000 003	99		(AF039038) Similar to acyl-coA dehydrogenase; coded for by C. elegans cDNA yk335a7.3; coded for by C. elegans cDNA yk335a7.5 [Caenorhabditis elegans]
17589	ENU01383	ANI61C1146 7:1156..660			TPEST	cluster1179_1					99		
17590	ENU01384	ANI61C7165: 1807..1218			TPEST	cluster4098_1		28	7.5		100		(AF080235) NDP-hexose synthetase homolog [Streptomyces cyanogenus]
17591	ENU01385	ANI61C39:40 6..865	24-45	171-198	TPEST	cluster523_1		31	1.9		99		(U22016) retinoid X receptor interacting protein [Mus musculus]
17592	ENU01386	ANI61C7486: 3090..3341	22-44	321-348	TPEST	cluster268_1					97		
17593	ENU01387	ANI61C2935: 231..571	58-85	299-318	TPEST	cluster9762_1		76	4E-15		100		(AL033388) putative 50s ribosomal protein 114 [Schizosaccharomyces pombe]
17594	ENU01388	ANI61C3288: 3409..2600	56-75	245-264	TPEST	cluster5614_1		35	0.12		100		guanine nucleotide-binding protein beta subunit-like protein (cross-pathway control WD-repeat protein CPC-2) ; CPC2 protein - Neurospora crassa ; (X81875) CPC2 protein [Neurospora crassa]
17595	ENU01389	ANI61C7805: 1055..1604			TPEST	cluster4513_1					99		
17596	ENU01390	ANI61C435:3 206..3889			TPEST	cluster344_1					98		
17597	ENU01391	ANI61C9395: 6602..5856			TPEST	cluster1755_1					99		
17598	ENU01392	ANI61C6804: 2458..1883			TPEST	cluster4647_1					100		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17599	ENU01393	ANI61C9397: 1369..1905	48-67	191-209	TPEST	cluster762_1			47	0.00007	98		hypothetical 52.5 KD protein ZK945.1 in chromosome II ; (Z48544) similar to esterase; cDNA EST EMBL:T02204 comes from this gene; cDNA EST EMBL:D68873 comes from this gene; cDNA EST yk206h6.3 comes from this gene; cDNA EST yk206h6.5 comes from this gene; cDNA EST yk299e8.3 comes from...
17600	ENU01394	ANI61C9409: 2370..2856			TPEST	cluster275_1					99		(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]
17601	ENU01395	ANI61C941:1 117..602			TPEST	cluster19_1		48	0.00001		100		(L40459) latent transforming growth factor-beta binding protein [Mus musculus]
17602	ENU01396	ANI61C9418: 1..948	22-43	167-194	TPEST	cluster7260_1			31	3.6	99		hypothetical 25.3 KD protein in PEX17-MER1 intergenic region ; hypothetical protein YNL213c - yeast (Saccharomyces cerevisiae) ; (X78898) N1323 [Saccharomyces cerevisiae] ; (Z71489) ORF YNL213c [Saccharomyces cerevisiae]
17603	ENU01397	ANI61C9422: 1802..1418	23-42	338-358	TPEST	cluster8272_1					100		
17604	ENU01398	ANI61C2251: 1305..817			TPEST	cluster3259_1			64	7E-10	100		
17605	ENU01399	ANI61C3368: 102-124 7485..8422	102-124	612-631	TPEST	cluster2767_1					99		
17606	ENU01400	ANI61C1026 8:597..1			TPEST	cluster658_1					99		
17607	ENU01401	ANI61C1194: 219..694			TPEST	cluster1975_1					99		
17608	ENU01402	ANI61C2364: 1747..1387			TPEST	cluster2952_1					98		
17609	ENU01403	ANI61C1111 6:1..415			TPEST	cluster902_1					96		
17610	ENU01404	ANI61C7935: 22-49 2554..2136	22-49	308-327	TPEST	cluster11415_1					99		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17611	ENU01405	ANI61C6091: 25-45 994..593	592-612	592-612	TPEST	cluster9842_1			130	1E-29	99		(U62929) multidrug resistance protein 1 [Filobasidiella neoformans] ; (U62930) multidrug resistance protein 1 [Filobasidiella neoformans] (AJ223999) PCZA363.3 [Amycolatopsis orientalis] (AF045014) translation release factor eRF3 [Podospora anserina]
17612	ENU01406	ANI61C9064: 347..1079	102-125	362-389	TPEST	cluster5610_1		31	6		99		
17613	ENU01407	ANI61C6422: 1679..2422			TPEST	cluster557_1		33	0.43		99		
17614	ENU01408	ANI61C6105: 1727..2188			TPEST	cluster1636_1					100		
17615	ENU01409	ANI61C2978: 22-49 237..71	188-215		TPEST	cluster4733_1		30	4		98		hypothetical 98.1 KD protein in ROM1-UPF3 intergenic region ; hypothetical protein YGR071c - yeast (Saccharomyces cerevisiae) ; (Z72856) ORF YGR071c [Saccharomyces cerevisiae]
17616	ENU01410	ANI61C6431: 232..511			TPEST	cluster515_1					100		
17617	ENU01411	ANI61C2449: 22-49 335..514	505-524		TPEST	cluster11421_1					99		
17618	ENU01412	"ANI61C7284 22-47 :721..486, ANI61C1056 5:749..344" "ANI61C4704 :422..899, ANI61C356:2 934..3239" "ANI61C1141 2:902..395, ANI61C6395: 515..28" "ANI61C4586 24-51 :1161..216, ANI61S160:3 09..1"	360-379		MCEST	"j9h03a1.r1, j9h03a1.fl"		31	4.4				ANI61CM23046
17619	ENU01413	"ANI61C4704 :422..899, ANI61C356:2 934..3239" "ANI61C1141 2:902..395, ANI61C6395: 515..28" "ANI61C4586 24-51 :1161..216, ANI61S160:3 09..1"			MCEST	"x8e05a1.r1, x8e05a1.fl"		39	0.012				ANI61CM12685
17620	ENU01414	"ANI61C1141 2:902..395, ANI61C6395: 515..28" "ANI61C4586 24-51 :1161..216, ANI61S160:3 09..1"			MCEST	"z5c08a1.r1, z5c08a1.fl"		34	0.66				(AL030978) putative protein [Arabidopsis thaliana]
17621	ENU01415	"ANI61C4586 24-51 :1161..216, ANI61S160:3 09..1"	241-266		MCEST	"x7d08a1.r1, x7d08a1.fl"		33	0.54				(Z81586) predicted using Genefinder [Caenorhabditis elegans]
17622	ENU01416	"ANI61C1556 62-89 :1871..2127, ANI61C6675: 1..370"	322-348		MCEST	"i3a04a1.r1, i3a04a1.fl"		42	0.002				(AB018284) KIAA0741 protein [Homo sapiens]

Gene Ontology

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17623	ENU01417	"ANI61C8655 :121..57, ANI61C3164: 444..1"	22-45	379-405	MCEST	"o0c11a1.r1, o0c11a1.fl"			50	0.000009			nuclear transport factor 2 (NTF-2) (nuclear transport factor P10) ; hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae] "elongation factor 2 (EF-2) ; (AE000876) translation elongation factor, EF-2 [Methanobacterium thermoautotrophicum] " (AL033388) hypothetical protein [Schizosaccharomyces pombe]
17624	ENU01418	"ANI61C4903 :2045..1437, ANI61C9734: 1268..873"			MCEST	"m6a10a1.r1, m6a10a1.fl"			30	7.2			
17625	ENU01419	"ANI61C9301 :796..1232, ANI61C7484: 1126..1653"	26-46	478-505	MCEST	"z3a11a1.r1, z3a11a1.fl"			99	1E-25			
17626	ENU01420	"ANI61C1051 :7:1421..1334, ANI61C9111: 1393..948"	22-44	397-424	MCEST	"n3e04a1.r1, n3e04a1.fl"			35	0.26			(AF129887) ORF1 protein [TT virus]
17627	ENU01421	"ANI61C6610 :965..1484, ANI61C3639: 1..432"			MCEST	"u4g08a1.r1, u4g08a1.fl"			32	2.8			(Z66565) cDNA EST EMBL:D70617 comes from this gene; cDNA EST EMBL:C10400 comes from this gene; cDNA EST EMBL:C10605 comes from this gene; cDNA EST EMBL:C12377 comes from this gene; cDNA EST EMBL:C13473 comes from this gene; cDN...
17628	ENU01422	"ANI61C5489 :579..491, ANI61C9734: 1237..873"	22-48	284-303	MCEST	"flh08a1.r1, flh08a1.fl"			30	6.2			ANI61CM30058
17629	ENU01423	"ANI61C8742 :1061..419, ANI61C1138 :6:661..194"	22-47	404-427	MCEST	"r5h03a1.r1, r5h03a1.fl"			36	0.16			(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
17630	ENU01424	"ANI61C2524 :253..465, ANI61C2973: 1974..2387"	23-42	287-306	MCEST	"k0a08a1.r1, k0a08a1.fl"			119	8E-27			ANI61CM52644

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Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17631	ENU01425	"ANI61C9187 :100..1, ANI61C1037 2:1443..1134"	53-80	262-288	MCEST	"k5d05a1.r1, k5d05a1.fl"			59	0.000000 008			ANI61CM33423
17632	ENU01426	"ANI61C6862 :705..1032, ANI61C8239: 2125..2608"	22-47	242-264	MCEST	"m0d07a1.r1, m0d07a1.fl"			31	5.7			ANI61CM29073
17633	ENU01427	"ANI61C8256 :1722..2265, ANI61C126:2 58..636"			MCEST	"r3h08a1.r1, r3h08a1.fl"			44	0.0005			30 KD heat shock protein ; heat-shock protein 30 - Emericella nidulans ; (D32070) heat-shock protein 30 (HSP30) [Emericella nidulans] ; heat shock protein 30 [Emericella nidulans] ANI61CM44025
17634	ENU01428	"ANI61C1102 9:1199..1584, ANI61C6494: 5368..5685"	23-47	269-296	MCEST	"m0h07a1.r1, m0h07a1.fl"			30	5			ANI61CM28276
17635	ENU01429	"ANI61C2451 :1000..1120, ANI61C5287: 2067..2417"			MCEST	"h0d12a1.r1, h0d12a1.fl"			32	1.2			
17636	ENU01430	"ANI61C8789 :1..645, ANI61C3400: 303..742"	22-42	398-417	MCEST	"i3f01a1.r1, i3f01a1.fl"			36	0.15			clathrin assembly protein AP180 short form - rat ; (X68877) assembly protein 180 (AP180) [Rattus norvegicus]
17637	ENU01431	"ANI61C7182 :227..700, ANI61C6591: 142..750"	41-65	563-587	MCEST	"n8a06a1.r1, n8a06a1.fl"			35	0.003			ANI61CM45211
17638	ENU01432	"ANI61C7673 :235..1652, ANI61C4595: 81..446"	22-46	321-344	MCEST	"y8h08a1.r1, y8h08a1.fl"			30	6.3			(L29246) UL103 homologue [Murine cytomegalovirus]
17639	ENU01433	"ANI61C9872 :1314..1216, ANI61C7232: 351..13"	23-42	219-238	MCEST	"n3c07a1.r1, n3c07a1.fl"			31	3.2			ANI61CM28370

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17640	ENU01434	"ANI61C1980 :217..579, ANI61C4162: 3806..4244"	65-91	390-417	MCEST	"n8b03a1.rl, n8b03a1.fl"			157	5E-38			"alpha-L-arabinofuranosidase precursor (arabinoxylan arabinofuranohydrolase) ; (Z78011) (1,4)-beta-D-arabinoxylan arabinofuranohydrolase [Aspergillus niger]"
17641	ENU01435	"ANI61C1899 :1460..1781, ANI61C5951: 259..563"	26-49	248-267	MCEST	"w5b10a1.rl, w5b10a1.fl"			30	5.9			(AL022244) hypothetical protein [Schizosaccharomyces pombe]
17642	ENU01436	"ANI61C7770 :1..323, ANI61C1069 5:105..432"	33-60	279-306	MCEST	"n3b02a1.rl, n3b02a1.fl"			52	0.000001			ANI61CM440121
17643	ENU01437	"ANI61C2219 :588..9, ANI61C426:3 52..1"	22-41	223-250	MCEST	"m6g01a1.rl, m6g01a1.fl"			116	4E-26			"1,4-alpha-glucan branching enzyme (glycogen branching enzyme) ; 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - yeast (Saccharomyces cerevisiae) ; (U18530) 1,4-alpha-glucan branching enzyme [Saccharomyces cerevisiae]"
17644	ENU01438	"ANI61C9501 :454..838, ANI61C8893: 4427..4742"	22-43	249-268	MCEST	"t2c07a1.rl, t2c07a1.fl"			31	4.1			ANI61CM4461
17645	ENU01439	"ANI61C6862 :94..483, ANI61C8239: 2117..2507"	22-49	250-272	MCEST	"b0h07a1.rl, b0h07a1.fl"			31	4.1			ANI61CM29073
17646	ENU01440	"ANI61C3773 :1028..754, ANI61C944:6 86..292"			MCEST	"c6c11a1.rl, c6c11a1.fl"			30	7.1			ANI61CM36375
17647	ENU01441	"ANI61C2967 :2121..2532, ANI61C4167: 1..395"	108-127	293-312	MCEST	"m7e11a1.rl, m7e11a1.fl"			31	5.5			(Y14459) polypeptide [porcine enterovirus 9]
17648	ENU01442	"ANI61C3279 :1318..868, ANI61C879:1 331..961"	22-49	320-339	MCEST	"w5g07a1.rl, w5g07a1.fl"			31	2.9			(AF054826) VAMP5 [Rattus norvegicus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17649	ENU01443	"ANI61C2870 :571..965, ANI61C4864: 2044..2382"	22-43	203-220	MCEST	"y4d10a1.r1, y4d10a1.fl"			30	5.5			74 KD serum albumin precursor ; 74K albumin precursor - African clawed frog
17650	ENU01444	"ANI61C8821 :2544..2217, ANI61C7328: 7157..6846"	22-47	225-244	MCEST	"w5b11a1.r1, w5b11a1.fl"			32	1.2			"(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA..." ANI61CM50706
17651	ENU01445	"ANI61C1113 :5:3232..2655, ANI61C2269: 1156..671"	60-79	420-447	MCEST	"g6e03a1.r1, g6e03a1.fl"			32	3.3			
17652	ENU01446	"ANI61C2394 :1035..773, ANI61C1739: 3030..2657"	24-48	307-326	MCEST	"d4h03a1.r1, d4h03a1.fl"			82	1E-15			"Glucoamylase, Granular Starch-Binding Domain, Nmr, Minimized Average Structure ; Glucoamylase, Granular Starch-Binding Domain, Nmr, 5 Structures ; Glucoamylase, Granular Starch-Binding Domain Complex With Cyclodextrin, Nmr, Minimized Average Structure ; Glucoamylase, Granular Starch-Binding Domain Complex With Cyclodextrin, Nmr, 5 Structures "
17653	ENU01447	"ANI61C7652 :1075..880, ANI61C3745: 566..169"	62-89	349-371	MCEST	"w6h06a1.r1, w6h06a1.fl"			36	0.096			(AC006283) hypothetical protein [Arabidopsis thaliana]
17654	ENU01448	"ANI61C1041 :3:279..1, ANI61C1174: 1038..617"			MCEST	"r7g11a1.r1, r7g11a1.fl"			35	0.31			(AE001393) phospholipase A2-like a/b fold hydrolase [Plasmodium falciparum]
17655	ENU01449	"ANI61C2737 :738..813, ANI61C1194: 348..683"	61-80	216-239	MCEST	"r1d10a1.r1, r1d10a1.fl"			33	0.63			(Z99162) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17656	ENU01450	"ANI61C7853 :2165..2592, ANI61C9581:693..1308"	35-54	571-594	MCEST	"c9h06a1.r1, c9h06a1.fl"			50	0.00001			urea amidolyase [Pichia jadinii]
17657	ENU01451	"ANI61C3856 :5281..5547, ANI61C4618:226..571"	29-48	304-324	MCEST	"c4c12a1.r1, c4c12a1.fl"		31	2.5				nucleolar protein p120 - mouse (fragment)
17658	ENU01452	"ANI61C9663 :2495..2828, ANI61C8533:570..1025"	22-45	408-429	MCEST	"r3a11a1.r1, r3a11a1.fl"		31	5.2				soluble vascular endothelial cell growth factor receptor - human ; (U01134)
17659	ENU01453	"ANI61C1007 :7:345..54, ANI61C6856:1302..921"	65-84	340-360	MCEST	"v3f04a1.r1, v3f04a1.fl"		30	6.8				soluble vascular endothelial cell growth factor receptor [Homo sapiens] (X70339) exon 2 [Saccharomyces cerevisiae]
17660	ENU01454	"ANI61C2394 :2893..3227, ANI61C6325:3137..3527"	57-84	346-367	MCEST	"c9f01a1.r1, c9f01a1.fl"		170	5E-53				probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740)
17661	ENU01455	"ANI61C8914 :293..604, ANI61S4152:1..407"	42-68	359-384	MCEST	"g3d06a1.r1, g3d06a1.fl"		31	5.7				putative p450 monooxygenase [Emericella nidulans] ANI61CM38315
17662	ENU01456	"ANI61C1010 :0:2843..2981, ANI61C7089:71..481"	22-45	362-389	MCEST	"o6b02a1.r1, o6b02a1.fl"							ANI61CM41145
17663	ENU01457	"ANI61C6597 :1..72, ANI61C3524:50..592"	60-87	332-353	MCEST	"j4f01a1.r1, j4f01a1.fl"		39	0.023				MOESIN ; (U14180) moesin [Lytechinus variegatus]
17664	ENU01458	"ANI61C6625 :201..1, ANI61C1899:1665..1262"	22-47	359-379	MCEST	"n3f02a1.r1, n3f02a1.fl"		117	3E-26				protein disulfide isomerase precursor (PDI) ; protein disulfide-isomerase (EC 5.3.4.1) - Aspergillus niger ; (X89449) protein disulfide isomerase [Aspergillus niger] ; (X98797) protein disulfide isomerase [Aspergillus niger]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17665	ENU01459	"ANI61C4700 :432..1, ANI61C1138 0:911..599"	22-49	268-287	MCEST	"h8f01a1.rl, h8f01a1.fl"			33	0.55			(Z99292) hypothetical protein [Schizosaccharomyces pombe]
17666	ENU01460	"ANI61C6726 :1200..1621, ANI61C4083: 99..417"	63-90	271-297	MCEST	"y3b09a1.rl, y3b09a1.fl"			30	5			ANI61CM52592
17667	ENU01461	"ANI61C9301 :798..1167, ANI61C9566: 1029..1512"	40-59	409-436	MCEST	"m6d04a1.rl, m6d04a1.fl"			34	0.86			(AF017250) vitellogenin precursor [Oreochromis aureus]
17668	ENU01462	"ANI61C2308 :840..543, ANI61C1899: 1653..1235"	22-45	365-384	MCEST	"m6b06a1.rl, m6b06a1.fl"			129	1E-29			protein disulfide isomerase precursor (PDI) ; protein disulfide-isomerase (EC 5.3.4.1) - Aspergillus niger ; (X89449) protein disulfide isomerase [Aspergillus niger] ; (X98797) protein disulfide isomerase [Aspergillus niger] ANI61CM33599
17669	ENU01463	"ANI61C1102 :9:691..1191, ANI61C346:2 933..3336"	22-45	360-382	MCEST	"f2b12a1.rl, f2b12a1.fl"			31	3.3			
17670	ENU01464	"ANI61C7184 :4690..4574, ANI61C9821: 6436..6132"	22-48	218-241	MCEST	"c6d06a1.rl, c6d06a1.fl"			205	2E-52			(U95045) velvet A [Emericella nidulans]
17671	ENU01465	"ANI61C6741 :1692..1918, ANI61C8333: 1318..1784"	27-54	421-440	MCEST	"u4c01a1.rl, u4c01a1.fl"			32	2.2			(D83390) connectin/titin [Gallus gallus]
17672	ENU01466	"ANI61C6814 :4164..3779, ANI61C971:4 473..4034"	22-46	382-401	MCEST	"d4h01a1.rl, d4h01a1.fl"			33	1.2			ANI61CM36803
17673	ENU01467	"ANI61C8310 :3802..3562, ANI61C1111 8:681..270"			MCEST	"z7h03a1.rl, z7h03a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17682	ENU01476	ANI61C4101: 450..870	97-114	456-475	NAP		g2117305	135	48	0.00004			(Z95620) putative dna binding protein [Schizosaccharomyces pombe]
17683	ENU01477	ANI61S3147: 506..23	109-130	531-550	NAP		g4512655	622	135	2.00E-54	84	45	(AC007048) putative protein phosphatase 2C [Arabidopsis thaliana]
17684	ENU01478	ANI61C893:3 352..4027	77-97	691-710	NAP		g1723528	504	73	1.00E-12	36	21	hypothetical 53.0 KD protein C22E12.17C in chromosome I ; (Z70043) unknown
17685	ENU01479	ANI61C9776: 69..1349	90-113	1310-1329	NAP		g3766375	124	81	2.00E-14	29	39	[Schizosaccharomyces pombe] "(AL031907) putative transcriptional regulation protein, trp-asp repeat containing [Schizosaccharomyces pombe] "
17686	ENU01480	ANI61C1110 7:10801..1114	65-84	345-365	NAP		g4455309	258	120	3.00E-27	47	48	(AL035528) hypothetical protein [Arabidopsis thaliana]
17687	ENU01481	ANI61C6001: 278..673	106-125	446-465	NAP		g2621995	463	128	2.00E-29	50	36	(AE000865) conserved protein [Methanobacterium thermoautotrophicum]
17688	ENU01482	ANI61S2131: 485..72	105-124	457-476	NAP		g731893	265	100	5.00E-21	35	25	putative transporter YIL166C ; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae]
17689	ENU01483	ANI61C8084: 5381..5797	115-134	470-489	NAP		g114959	609	114	3.00E-25	48	18	Thermotable beta-glucosidase B (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) B - Clostridium thermocellum ; (X15644) bglB gene (AA1-754) [Clostridium thermocellum]

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17690	ENU01484	ANI61C2517: 1000..557	42-64	424-443	NAP		g125727	247	84	2.00E-16			Killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URFP2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
17691	ENU01485	ANI61C5196: 111-130 563-582 1189..676			NAP		g549674	586	70	1.00E-11			hypothetical 49.6 KD protein in ELM1-PR12 intergenic region ; hypothetical protein YKL046c precursor - yeast (Saccharomyces cerevisiae) ; (Z28046) ORF YKL046c [Saccharomyces cerevisiae]
17692	ENU01486	ANI61C7556: 94-113 4782..4141		670-693	NAP		g2408015	246	51	0.000009	33	57	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
17693	ENU01487	ANI61C922:1 46-65 034..354		663-684	NAP		g1705437	538	126	5.00E-39	50	51	"Branched-chain amino acid aminotransferase, cytosolic (BCAT) (ECA39 protein) ; (U42443) MECA39 [Mus musculus] "
17694	ENU01488	ANI61C1319: 34-55 184..947		735-755	NAP		g3328190		42	0.004			(AF074266) proto-oncogene AF4 [Mus musculus]
17695	ENU01489	ANI61C8803: 54-76 1587..1194		1546-1567	NAP		g3121869		171	1.00E-41	42	30	Coronin-like protein ; (Z99753) hypothetical protein [Schizosaccharomyces pombe]
17696	ENU01490	ANI61C5193: 118-140 2113-2292..233			NAP		g1166378	784	252	2.00E-77	34	59	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
17697	ENU01491	ANI61S4436: 31-51 133..426		262-282	NAP								
17698	ENU01492	ANI61C8712: 122-141 171..491		383-400	NAP		g339913		42	0.001			peripheral-type benzodiazepine receptor 1 isoquinoline-binding protein - mouse ; (D21207) peripheral-type benzodiazepine receptor [Mus musculus]
17699	ENU01493	ANI61C5155: 100-120 3236..2870		404-423	NAP		g1399020	154	36	0.000004			(U34658) FKIF6 [Morone saxatilis]

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17700	ENU01494	ANI61C7145: 2421..1716	114-131	756-777	NAP		g3885836	128	44	0.001	33	18	putative cercosporin transporter [Cercospora kikuchii] (Y18476) NADH dehydrogenase subunit 2 [Trichophyton rubrum] Polyketide synthase HETM; hetM protein - Anabaena sp. (PCC 7120); (L22883) polyketide synthase [Anabaena sp.]
17701	ENU01495	ANI61C1089 0:940..579	24-49	757-788	NAP		g3947740	1043	217	1.00E-55	67	47	cell division control protein 25; SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment); (M82964) CDC25 [Saccharomyces kluyveri]
17702	ENU01496	ANI61C5157: 85..1080	25-44	959-978	NAP		g585251	297	146	2.00E-34	29	62	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" "(AL031535) putative transcription factor subunit, TPR domain [Schizosaccharomyces pombe]" (AC004793) Strong similarity to gi 3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb AF080119 and is a member of the reverse transcriptase family PF 00078.
17703	ENU01497	ANI61C1117: 6205..9180	102-121	3016-3035	NAP		g399198	335	103	7.00E-41	28	26	(AL022117) putative o-methyltransferase [Schizosaccharomyces pombe] (Y09020) fructosyl amino acid oxidase [Aspergillus terreus] (AB012580) eIF3 p66 [Mus musculus] (X05615) thyroglobulin [Homo sapiens] (AL023286) probable atp-dependent rna helicase [Schizosaccharomyces pombe] (U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis]
17704	ENU01498	ANI61C7188: 5879..2904	111-129	3027-3045	NAP		g1166378	828	393	e-111	32	87	
17705	ENU01499	ANI61C1137 7:131..3117	85-104	3010-3029	NAP		g3560268	538	141	4.00E-64	28	86	
17706	ENU01500	ANI61C3679: 5946..2954	104-123	3035-3054	NAP		g4512618	665	245	3.00E-92	28	61	
17707	ENU01501	ANI61C1132 1:726..375	122-142	412-431	NAP		g2959364		74	4.00E-13			
17708	ENU01502	ANI61C6286: 2070..2522	91-109	477-501	NAP		g1653970	196	68	4.00E-11	33	33	
17709	ENU01503	ANI61S4271: 5..510	26-49	461-489	NAP		g2992164	491	179	1.00E-44	51	30	
17710	ENU01504	ANI61C3193: 578..58	122-144	579-600	NAP		g37174		42	0.003			
17711	ENU01505	ANI61C9970: 1873..1332	117-138	629-648	NAP		g3116113	534	150	5.00E-36	46	26	
17712	ENU01506	ANI61C2497: 2277..3199	121-142	981-1000	NAP		g1658175	673	117	1.00E-47	41	56	

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17713	ENU01507	ANI61C9216: 1258..94	98-117	1202-1220	NAP		g2132247	517	201	8.00E-51	33	40	hypothetical protein YPL249c - yeast (Saccharomyces cerevisiae) ; (Z67751) putative protein [Saccharomyces cerevisiae] ; (Z73605) ORF YPL249c [Saccharomyces cerevisiae]
17714	ENU01508	ANI61C3460: 3079..1846	99-120	1271-1290	NAP		g2131417	996	337	7.00E-92	48	33	hypothetical protein YDR291w - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr291wp [Saccharomyces cerevisiae]
17715	ENU01509	ANI61C6244: 80..1353	88-108	1298-1319	NAP		g2498440	2193	734	0	98	87	"homogentisate 1,2-dioxygenase (homogentisicase) (homogentisate oxygenase) (homogentisic acid oxidase) ; 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) - Emericella nidulans ; (U30797) 2,5 dihydroxyphenylacetate oxidase [Emericella nidulans] ; (AJ001836) homogentisate dioxygenase [Emericella nidulans]"
17716	ENU01510	ANI61C7285: 4043..7025	109-128	3029-3049	NAP		g1723934	133	89	2.00E-16	27	51	hypothetical 41.6 KD protein in SUT1-RCK1 intergenic region ; probable membrane protein YGL159w - yeast (Saccharomyces cerevisiae) ; (Z72681) ORF YGL159w [Saccharomyces cerevisiae]
17717	ENU01511	ANI61C1056 0:80..269	68-87	225-244	NAP		g3169094	215	71	1.00E-12	41	28	(AL023706) small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
17718	ENU01512	ANI61C813:3 88..65	71-90	333-352	NAP		g3299812	206	82	1.00E-15	51	87	(AB016006) ribosomal protein S31 homolog [Schizosaccharomyces pombe] ; (Z95620) 40s ribosomal protein s25 [Schizosaccharomyces pombe]
17719	ENU01513	ANI61C1510: 2260..1915	68-87	351-370	NAP		g4469025	158	69	8.00E-12	47	66	(AL035602) putative protein [Arabidopsis thaliana]
17720	ENU01514	ANI61C2772: 445..48	57-76	393-412	NAP		g2780359	462	141	2.00E-33	53	23	(AB010110) ascorbate oxidase [Acremonium sp.]
17721	ENU01515	ANI61C9732: 2295..1884	44-61	394-413	NAP		g2924502	625	32	2			(AL022019) lim domain protein [Schizosaccharomyces pombe]

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17731	ENU01525	ANI61S3483: 24-43	24-43	489-510	NAP		g3402674	751	233	7.00E-61	87	37	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]
17732	ENU01526	ANI61C7029: 72-91	72-91	559-578	NAP		g1169238	935	119	2.00E-44	61	31	"glutamate decarboxylase (GAD) ; glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia ; (L16797) glutamate decarboxylase [Petunia hybrida] ; (L16977) glutamate decarboxylase [Petunia hybrida] "
17733	ENU01527	ANI61C9584: 56-75	56-75	553-572	NAP		g1103515	217	91	6.00E-18	36	86	(Z68144) hypothetical protein [Schizosaccharomyces pombe]
17734	ENU01528	ANI61C1404: 65-84	65-84	564-583	NAP		g1169878		62	0.000000			GTP cyclohydrolase II ; GTP cyclohydrolase II (ribA) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32706) GTP cyclohydrolase II (ribA) [Haemophilus influenzae Rd]
17735	ENU01529	ANI61C9912: 59-78	59-78	565-583	NAP		g130720	550	177	4.00E-50	71	71	proteolipid protein PPA1 ; probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) ; (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] ; (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae] (AF021234) 3-oxoacyl-[acyl-carrier-protein]-synthase [Neurospora crassa] (AF072709) unknown [Streptomyces lividans]
17736	ENU01530	ANI61C1043	22-42	535-554	NAP		g2522482	1231	107	3.00E-30	54	39	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
17737	ENU01531	ANI61C5523: 22-44	22-44	541-560	NAP		g3293539	216	83	1.00E-15	55	46	(AL035536) putative rna maturation protein [Schizosaccharomyces pombe]
17738	ENU01532	ANI61C9745: 32-51	32-51	589-612	NAP		g3169083	212	45	0.0006	38	36	
17739	ENU01533	ANI61C5924: 51-69	51-69	624-643	NAP		g4455778	860	100	8.00E-21			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17740	ENU01534	ANI61C8278: 22-42 809..149	22-42	621-640	NAP		g729566	1081	188	1.00E-48	57	41	"Secretory pathway GDP dissociation inhibitor ; GDP dissociation inhibitor GDI1 - yeast (Saccharomyces cerevisiae) ; (S69371) Gdi1p=GDP dissociation inhibitor [Saccharomyces cerevisiae, Peptide, 451 aa] [Saccharomyces cerevisiae] ; (U18916) Gdi1p: secretory pathway GDP dissociation inhibitor [Saccharomyces cerevisiae]"
17741	ENU01535	ANI61C8347: 39-58 693..1361	39-58	646-665	NAP		g1170136	449	200	7.00E-51	49	78	"endoglucanase V precursor (endo-1,4-beta-glucanase V) (cellULase V) (EGV) ; cellulase (EC 3.2.1.4) V precursor - fungus (Trichoderma reesei) (strain QM9414) ; (Z33381) endo-1,4-beta-glucanase V (EGV) [Hypocrea jecorina]"
17742	ENU01536	ANI61C1482: 59-78 918..1587	59-78	667-686	NAP		g4262216	491	170	9.00E-42	36	77	(AC006161) putative DNA binding protein [Arabidopsis thaliana]
17743	ENU01537	ANI61C3946: 42-61 1682..2371	42-61	670-689	NAP		g2104460	645	81	9.00E-15	40	20	(Z95397) unknown [Schizosaccharomyces pombe]
17744	ENU01538	ANI61C3736: 50-69 2629..1923	50-69	695-714	NAP		g461623	334	65	6.00E-10	31	23	"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]"
17745	ENU01539	ANI61C842:1 72-91 216..1938	72-91	733-752	NAP		g1514667	227	79	5.00E-19	34	59	(X92509) erg1 [Ustilago maydis]
17746	ENU01540	ANI61C405:1 32-52 53..958	32-52	778-795	NAP		g3219304	1070	183	2.00E-75	69	25	(AB009461) MUS38 [Neurospora crassa]
17747	ENU01541	ANI61C1420: 57-76 36..853	57-76	813-832	NAP		g3913051	244	76	1.00E-20	31	54	putative flavin-containing monoamine oxidase MTV014.14 ; (AL021646) hypothetical protein Rv3170 [Mycobacterium tuberculosis]
17748	ENU01542	ANI61C4648: 47-66 1263..2101	47-66	824-843	NAP		g2389003	1358	264	7.00E-80	60	33	(Z98981) hypothetical protein [Schizosaccharomyces pombe]
17749	ENU01543	ANI61C7922: 22-44 1708..829	22-44	837-856	NAP		g3264834	341	71	1.00E-20	30	74	(AF072541) xyitol dehydrogenase; XDH [Galactocandida mastotermis]
17750	ENU01544	ANI61C7526: 39-58 1573..2457	39-58	855-881	NAP		g3661541	166	48	0.00007	31	77	(AF091396) poly-zinc finger protein [Trypanosoma cruzi]

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17751	ENU01545	ANI61C9518: 1440..545	71-90	904-923	NAP		g2132224	294	89	4.00E-17	31	66	hypothetical protein YPL191c - yeast (Saccharomyces cerevisiae) ; (Z73547) ORF YPL191c [Saccharomyces cerevisiae]
17752	ENU01546	ANI61C6095: 46..951	66-89	910-929	NAP		g1351702	289	66	5.00E-10	26	54	hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
17753	ENU01547	ANI61C9283: 2904..3829	65-84	929-948	NAP		g3183125	1148	369	e-101	55	67	probable DNA PRIMase small subunit ; (Z98531) hypothetical dna primase [Schizosaccharomyces pombe]
17754	ENU01548	ANI61C8752: 1075..142	47-67	919-938	NAP		g2257527	452	91	9.00E-18	43	63	[Schizosaccharomyces pombe] (AB004537) HLI1 protein
17755	ENU01549	ANI61C1824: 1124..169	51-70	945-964	NAP		g3764057	623	257	6.00E-68	45	75	[Schizosaccharomyces pombe] (AF016246) purine nucleoside permease [Candida albicans]
17756	ENU01550	ANI61C1534: 2451..1488	22-41	918-937	NAP		g729859	1735	294	1.00E-82	49	40	Sexual differentiation process protein ISP4 ; isp4 protein - fission yeast (Schizosaccharomyces pombe) ; (D14061) ORF [Schizosaccharomyces pombe]
17757	ENU01551	ANI61C7241: 4535..3565	26-45	935-954	NAP		g3006143	98	52	0.000005	42	25	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
17758	ENU01552	ANI61C8537: 14838..15811	33-52	945-964	NAP		g2665358	551	173	2.00E-42	30	40	(Y15774) copper amine oxidase [Bos taurus]
17759	ENU01553	ANI61C1033: 5:2249..3254	29-47	970-992	NAP		g416590	937	288	5.00E-77	51	38	AFG2 protein ; valosin-containing protein homolog AFG2 - yeast (Saccharomyces cerevisiae) ; (L14615) AFG2 [Saccharomyces cerevisiae] ; (U19729) Afg2p [Saccharomyces cerevisiae]
17760	ENU01554	ANI61C9762: 2023..1017	69-90	1013-1033	NAP		g950007		52	0.000005			(U26938) Tc1-like transposase [Drosophila virilis] ; (Z49253) Tc1-like transposase [Drosophila virilis]
17761	ENU01555	ANI61C2412: 1302..294	35-54	982-1001	NAP		g2981103	512	101	1.00E-20	32	26	(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]

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17762	ENU01556	ANI61C8543: 23-42 4912..5920		970-989	NAP		g2388955	1037	253	7.00E-87	64	77	(Z98979) putative isopropyl malate dehydrogenase [Schizosaccharomyces pombe]
17763	ENU01557	ANI61C5900: 70-89 1169..84	1094-1113		NAP		g3080523	1115	398	e-110	58	67	(AL022599) aspartate kinase [Schizosaccharomyces pombe]
17764	ENU01558	ANI61C1047 23-48 0:5194..4079	1078-1097		NAP		g2414638	623	185	2.00E-54	43	70	(Z99260) putative microsomal dipeptidase precursor [Schizosaccharomyces pombe]
17765	ENU01559	ANI61C7992: 60-81 1138..7	1130-1149		NAP		g3881525	227	112	5.00E-24	28	14	(Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene [Caenorhabditis elegans]
17766	ENU01560	ANI61C6916: 71-90 50..1183	1143-1162		NAP		g3080530	294	96	3.00E-19	38	30	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
17767	ENU01561	ANI61C1110 22-41 5:2100..901	1161-1179		NAP		g730701	1749	347	e-137	79	77	adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (ADOHCYase); adenosylhomocysteinase (EC 3.3.1.1) - yeast (Saccharomyces cerevisiae); (U18796) Sam1p: Adenosylhomocysteinase [Saccharomyces cerevisiae]
17768	ENU01562	ANI61C9449: 47-66 75..1367	1278-1298		NAP		g1730731	1037	288	2.00E-94	49	46	hypothetical 98.9 KD protein in COX5A-ALG11 intergenic region; hypothetical protein YNL049c - yeast (Saccharomyces cerevisiae); (U12141) Ynl2505p [Saccharomyces cerevisiae]; (Z71325) ORF YNL049c [Saccharomyces cerevisiae]; (AJ009783) Sfb2 [Saccharomyces cerevisiae]
17769	ENU01563	ANI61C919:4 67-86 6..1389	1349-1368		NAP		g3236468	1583	593	e-169	69	58	(AF070481) minichromosome maintenance protein Mcm7p [Schizosaccharomyces pombe]; (AL031158) yeast cell division control protein 47 homologue [Schizosaccharomyces pombe]

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17770	ENU01564	ANI61C7722: 1954..528	26-45	1390-1410	NAP		g3915458	1728	458	e-154	65	62	putative ABC transporter C8C9.18 in chromosome I
17771	ENU01565	ANI61C4806: 58-77		1433-1452	NAP		g2239229	2162	761	0	82	84	(Z97210) hypothetical protein [Schizosaccharomyces pombe]
17772	ENU01566	ANI61C1059: 24-45		1410-1429	NAP		g172707	811	193	6.00E-89	47	56	(M77274) SRP receptor alpha-chain homologue [Saccharomyces cerevisiae]
17773	ENU01567	1:206..1652 ANI61C385:5 51-70 16..1996		1470-1489	NAP		g1709487	945	372	e-102	54	59	"Origin recognition complex protein, subunit 1 ; (U38522) Orp1 [Schizosaccharomyces pombe] ; (U40378) orc1+ protein [Schizosaccharomyces pombe] ; (AL034463) origin recognition complex protein, subunit 1. [Schizosaccharomyces pombe] "
17774	ENU01568	ANI61C630:2 38-58 511..963		1525-1544	NAP		g4154090	329	75	2.00E-21	37	79	(Z99568) putative trna protein transferase [Schizosaccharomyces pombe]
17775	ENU01569	ANI61C7964: 64-84 3706..1944		1766-1784	NAP		g3023956	614	259	2.00E-74	38	30	Vegetative incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
17776	ENU01570	ANI61C7672: 63-82 788..2722		1936-1955	NAP		g2414651	665	207	2.00E-52	40	51	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
17777	ENU01571	ANI61C1035 45-64 2:2811..869		1926-1945	NAP		g4455171	305	148	2.00E-34	35	24	(AL035521) hypothetical protein [Arabidopsis thaliana]
17778	ENU01572	ANI61C1014 25-44 1:3168..1121		2011-2030	NAP		g3242651	2185	724	0	63	72	(AB015509) beta-mannosidase [Aspergillus aculeatus]
17779	ENU01573	ANI61C945:4 35-54 30..19		2049-2068	NAP		g2645229	388	167	3.00E-40	36	32	(U78597) kinesin light chain [Plectonema boryanum]
17780	ENU01574	ANI61C945:4 35-54 30..19		2049-2068	NAP		g2645229	388	167	3.00E-40	36	32	(U78597) kinesin light chain [Plectonema boryanum]
17781	ENU01575	ANI61C6394: 53-72 1991..2123		2078-2101	NAP		g3341488	853	367	e-100	42	75	(X99280) protein kinase [Schizosaccharomyces pombe] ; (AL031798) protein kinase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17782	ENU01576	ANI61C4040: 2608..2210	69-91	2106-2125	NAP		g586542	939	310	e-104	43	70	general amino acid permease AGP2; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae); (X75891) YBR1007 [Saccharomyces cerevisiae]; (Z36001) ORF YBR132c [Saccharomyces cerevisiae]; YBR1007 gene [Saccharomyces cerevisiae] (M77661) putative pol polyprotein [Magnaporthe grisea] Formamidase (formamide amidohydrolase); (X99632) formamidase [Methylophilus methylotrophus] Choline transport protein; choline transport protein - yeast (Saccharomyces cerevisiae); (J05603) choline transport protein [Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
17783	ENU01577	ANI61C554:3 698..1810	22-47	2187-2204	NAP		g538067	827	324	2.00E-87	33	39	hypothetical 90.6 KD protein C1D4.10 in chromosome I; (Z69239) unknown [Schizosaccharomyces pombe] (AE000913) conserved protein [Methanobacterium thermoautotrophicum] (AC000133) G5P19 [Emericella nidulans] (AJ011297) hypothetical protein [Emericella nidulans] 1-aminocyclopropane-1-carboxylate synthase 2 (ACC synthase 2) (S-adenosyl-L-methionine methylthioadenosine-lyase 2) (ACS-2); 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - tomato; (X59139) 1-aminocyclopropane 1-carboxylate synthase [Lycopersicon esculentum]
17784	ENU01578	ANI61C2603: 30-49 2357..58	30-49	2263-2287	NAP		g3913682	563	239	5.00E-62	56	29	
17785	ENU01579	ANI61C7999: 33-52 4536..2130	33-52	2378-2397	NAP		g117619		55	6.00E-14			
17786	ENU01580	ANI61C8896: 27-47 2811..248	27-47	2526-2545	NAP		g1723232	404	89	2.00E-16	27	87	
17787	ENU01581	ANI61C7000: 54-73 328..88	54-73	233-252	NAP		g2622649	174	73	5.00E-13	40	61	
17788	ENU01582	ANI61S1911: 71-91 293..32	71-91	272-290	NAP		g1870211	533	87	3.00E-17	94	71	
17789	ENU01583	ANI61C6801: 67-86 1072..783	67-86	295-314	NAP		g3647374	246	38	0.000002	80	67	
17790	ENU01584	ANI61C9457: 64-94 1374..1678	64-94	307-326	NAP		g584682	184	50	0.000005			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17791	ENU01585	ANI61C1107 3:11524..1185	70-89	340-363	NAP		g731476	441	169	6.00E-42	69	86	hypothetical 14.4 KD protein in RNR1-ALD3 intergenic region ; hypothetical protein YER072w - yeast (Saccharomyces cerevisiae) ; (U18813) Yer072wp [Saccharomyces cerevisiae] hypothetical 16.6 KD protein in THI5-AGP3 intergenic region ; hypothetical protein YFL057c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL057C [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae] nucleoside diphosphate kinase (NDK) (NDP kinase) ; nucleoside-diphosphate kinase (EC 2.7.4.6) - yeast (Saccharomyces cerevisiae) ; (X75780) A153 [Saccharomyces cerevisiae] ; (D13562) nucleoside diphosphate kinase [Saccharomyces cerevisiae] ; (Z28067) ORF YKL067w [Saccharomyces cerevisiae] ; nucleoside diphosphate kinase [Saccharomyces cerevisiae] (AF058825) contains similarity to human OS-9 precursor (GB:U41635) [Arabidopsis thaliana] (D64004) hypothetical protein [Synecocystis sp.] hypothetical 11.3 KD protein in MIR1-STE18 intergenic region ; probable membrane protein YJR085c - yeast (Saccharomyces cerevisiae) ; (Z49585) ORF YJR085c [Saccharomyces cerevisiae] ; (L47993) ORF YJR085c [Saccharomyces cerevisiae] "NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 14K chain - Neurospora crassa ; (Z18945) NADH:ubiquinone oxidoreductase (NADH dehydrogenase),14 kDa [Neurospora crassa]"
17792	ENU01586	ANI61C7942: 51-72 923..572	51-72	341-360	NAP		g1175961	493	156	4.00E-38	64	77	
17793	ENU01587	ANI61C584:8 08..1165	44-65	337-358	NAP		g548341	437	121	2.00E-27			
17794	ENU01588	ANI61C720:2 867..3240	22-53	333-352	NAP		g3047065	158	39	0.013			
17795	ENU01589	ANI61C4190: 61-82 2037..1658	61-82	371-398	NAP		g1208451	217	59	0.000000	27	36	
17796	ENU01590	ANI61C9077: 24-55 3225..2844	24-55	338-363	NAP		g1352897	174	59	4.00E-12	40	100	
17797	ENU01591	ANI61C3388: 23-46 1278..1659	23-46	343-362	NAP		g630424	222	76	1.00E-13	44	90	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17818	ENU01612	ANI61C6328: 52-71 1723..2180	52-71	436-467	NAP		g586336		59	0.000000 02			hypothetical 21.1 KD protein in HPC2-PYC2 intergenic region ; probable membrane protein YBR217w - yeast (Saccharomyces cerevisiae) ; (Z36086) ORF YBR217w [Saccharomyces cerevisiae] ; (AB017924) ORF YBR217w [Saccharomyces cerevisiae]
17819	ENU01613	ANI61C1006 59-79 3:598..1055	59-79	456-474	NAP		g586294	220	104	4.00E-22	34	48	hypothetical 35.8 KD protein in YSW1-RIB7 intergenic region ; hypothetical protein YBR151w - yeast (Saccharomyces cerevisiae) ; (Z36020) ORF YBR151w [Saccharomyces cerevisiae]
17820	ENU01614	ANI61C1122 31-52 3:562..100	31-52	433-451	NAP		g493580	1071	156	9.00E-38	51	20	(U09580) beta-D-glucoside glucosylhydrolase [Trichoderma reesei]
17821	ENU01615	ANI61C9892: 61-80 2016..1553	61-80	463-482	NAP		g3913210	591	211	2.00E-54	68	15	putative ATP-dependent RNA helicase CDC28 ; (U48733) Cdc28p [Schizosaccharomyces pombe]
17822	ENU01616	ANI61C6:504 22-46 ..38	22-46	427-446	NAP		g3218393	167	62	1.00E-12	38	43	(AL023860) short chain dehydrogenase [Schizosaccharomyces pombe]
17823	ENU01617	ANI61C2355: 66-85 591..124	66-85	472-491	NAP		g3395584	301	83	1.00E-15	31	12	(AL031179) importin beta subunit [Schizosaccharomyces pombe]
17824	ENU01618	ANI61S336:5 69-94 15..47	69-94	465-495	NAP		g4467143	761	268	1.00E-71	98	30	(AL035540) Phospholipase like protein [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17825	ENU01619	ANI61C4983: 841..371	31-54	436-459	NAP		g2392291	311	96	2.00E-19			"Chain A, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain B, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain C, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain D, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain E, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain F, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain A, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain B, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain C, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain D, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain E, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain F, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA"
17826	ENU01620	ANI61C8671: 1667..2137	22-51	431-450	NAP		g1172532	295	45	3.00E-10			penicillolysin precursor (deuterolysin) ; penicillolysin - Penicillium citrinum ; (D25535) Penicillolysin [Penicillium citrinum]
17827	ENU01621	ANI61C7181: 3922..4392	22-55	431-450	NAP		g3916	334	74	7.00E-13	33	35	(X66371) MDM1-protein [Saccharomyces cerevisiae]
17828	ENU01622	ANI61C1034 7:1930..1457	22-53	421-453	NAP		g1705681	1089	172	1.00E-42	51	23	cell division control protein 4 ; (X96763) CDC4 [Candida albicans]
17829	ENU01623	ANI61C1052 4:549..72	44-64	452-478	NAP		g1711582	291	124	3.00E-28	53	87	succinyl-CoA synthetase beta chain (SCS-beta) ; sucC succinyl-coA synthetase beta-chain - Pseudomonas aeruginosa (fragment) ; (X84052) succinyl-coA synthetase beta-subunit from sucC [Pseudomonas aeruginosa]
17830	ENU01624	ANI61C9832: 2367..1890	59-78	470-494	NAP		g548509	1100	211	2.00E-54	95	48	"possible phosphate-non-repressible acid phosphatase precursor ; acid phosphatase, 35.6K - Emericella nidulans ; (M96993) acid phosphatase [Emericella nidulans]"